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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION

(57) Abstract: Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SMP genes in this organism.

***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS
INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION**

Related Applications

- 5 This application claims priority to prior U.S. Provisional Patent Application
Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial
No. 60/143208, filed July 9, 1999, and U.S. Provisional Patent Application Serial No.
60/151572, filed August 31, 1999. This application also claims priority to prior German
Patent Application No. 19931412.8, filed July 8, 1999, German Patent Application No.
10 19931413.6, filed July 8, 1999, German Patent Application No. 19931419.5, filed July
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German Patent Application No. 19942125.0, filed September 3, 1999. The entire
30 contents of all of the aforementioned application are hereby expressly incorporated
herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

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Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as sugar metabolism and oxidative phosphorylation (SMP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SMP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. Modulation of the expression of the SMP nucleic acids of the invention, or modification of the sequence of the SMP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a

microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The SMP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the
5 presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain
10 whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SMP nucleic acid molecules of the invention may also serve as reference
15 points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The SMP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism of carbon
20 compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama
25 *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a
30 direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to compounds containing high energy phosphate bonds via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical. Also, many of the degradation products produced during sugar metabolism are utilized by the cell as precursors or intermediates in the production of other desirable products, such as fine chemicals. So, by increasing the ability of the cell to metabolize
5 sugars, the number of these degradation products available to the cell for other processes should also be increased.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as SMP proteins, which are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars and the
10 generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Nucleic acid molecules encoding an SMP protein are referred to herein as SMP nucleic acid molecules. In a preferred embodiment, the SMP protein participates in the conversion of carbon molecules and degradation products thereof to energy which is utilized by the cell for metabolic processes. Examples of
15 such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (e.g., cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SMP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SMP-
20 encoding nucleic acid (e.g., DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the
25 isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,
30 SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (e.g., SEQ ID NO:2, SEQ ID NO:4, SEQ

ID NO:6, SEQ ID NO:8....). The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence
5 which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SMP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform a function
10 involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%,
15 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-
20 numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SMP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of
25 the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also
30 includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing) A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SMP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SMP protein by culturing the host cell in a suitable medium. The SMP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SMP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SMP sequence as a transgene. In another embodiment, an endogenous SMP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SMP gene. In another embodiment, an endogenous or introduced SMP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 782) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SMP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the

5 isolated SMP protein or portion thereof is capable of performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In another preferred embodiment, the isolated SMP protein or portion thereof is sufficiently homologous to an amino acid sequence of the

10 invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

15 The invention also provides an isolated preparation of an SMP protein. In preferred embodiments, the SMP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention

20 (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous

25 to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SMP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to perform a function involved in the

30 metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SMP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 5 95%, 96%, 97%, 98,%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of SMP proteins also have one or more of the SMP bioactivities described herein.

The SMP polypeptide, or a biologically active portion thereof, can be operatively 10 linked to a non-SMP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SMP protein alone. In other preferred embodiments, this fusion protein performs a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in 15 *Corynebacterium glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a 20 substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SMP nucleic acid molecule of the invention, such that a fine chemical 25 is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SMP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or 30 *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an

agent which modulates SMP protein activity or SMP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* carbon metabolism pathways or for the production of energy through processes such as oxidative phosphorylation, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SMP protein activity can be an agent which stimulates SMP protein activity or SMP nucleic acid expression. Examples of agents which stimulate SMP protein activity or SMP nucleic acid expression include small molecules, active SMP proteins, and nucleic acids encoding SMP proteins that have been introduced into the cell. Examples of agents which inhibit SMP activity or expression include small molecules and antisense SMP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SMP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SMP nucleic acid and protein molecules which are involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (e.g., where overexpression or optimization of a glycolytic pathway protein has a direct impact on the yield, production, and/or efficiency of production of, e.g., pyruvate from modified *C. glutamicum*), or may have an indirect

impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (e.g., where modulation of proteins involved in oxidative phosphorylation results in alterations in the amount of energy available to perform necessary metabolic processes and other cellular functions, such as nucleic acid
5 and protein biosynthesis and transcription/translation). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by
10 an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described e.g. in Kuninaka, A. (1996) Nucleotides and
15 related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (e.g., arachidonic acid), diols (e.g., propane diol, and butane diol), carbohydrates (e.g., hyaluronic acid and trehalose), aromatic compounds (e.g., aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of
20 Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes,
25 polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

30 A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-

recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

5 Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids
10 (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals
15 do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical
20 industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine,
25 valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be
30 useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others

described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

- The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial
- 5 amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-
- 10 step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transfer of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate
- 15 pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all
- 20 biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.
- 25 Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in
- 30 terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own

production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

5

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are
10 either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications
15 of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor"
20 includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty
25 acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley
30 & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological

Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (*e.g.*, pyridoxine, pyridoxamine, pyridoxal-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), panthetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system.

The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD
5 (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and
10 biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

15 Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a
20 pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA
25 synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical
30 indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of

enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Sugar and Carbon Molecule Utilization and Oxidative Phosphorylation

Carbon is a critically important element for the formation of all organic compounds, and thus is a nutritional requirement not only for the growth and division of *C. glutamicum*, but also for the overproduction of fine chemicals from this microorganism. Sugars, such as mono-, di-, or polysaccharides, are particularly good carbon sources, and thus standard growth media typically contain one or more of: glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch, or cellulose (Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim). Alternatively, more complex forms of sugar may be utilized in the media, such as molasses, or other by-products of sugar refinement. Other compounds aside from the sugars may be used as alternate carbon sources, including alcohols (*e.g.*, ethanol or methanol), alkanes, sugar alcohols, fatty acids, and organic acids (*e.g.*, acetic acid or lactic acid). For a review of carbon sources and their utilization by microorganisms in culture, see: Ullman's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim; Stoppok, E. and Buchholz, K. (1996) "Sugar-based raw materials for fermentation applications" in Biotechnology (Rehm, H.J. *et al.*, eds.) vol. 6, VCH: Weinheim, p. 5-29; Rehm, H.J. (1980) *Industrielle Mikrobiologie*, Springer: Berlin; Bartholomew, W.H., and Reiman, H.B. (1979). Economics of Fermentation Processes, in: Peppler, H.J. and Perlman, D., eds. *Microbial Technology* 2nd ed., vol. 2, chapter 18, Academic Press: New York; and

Kockova-Kratachvilova, A. (1981) Characteristics of Industrial Microorganisms, in: Rehm, H.J. and Reed, G., eds. Handbook of Biotechnology, vol. 1, chapter 1, Verlag Chemie: Weinheim.

After uptake, these energy-rich carbon molecules must be processed such that they are able to be degraded by one of the major sugar metabolic pathways. Such pathways lead directly to useful degradation products, such as ribose-5-phosphate and phosphoenolpyruvate, which may be subsequently converted to pyruvate. Three of the most important pathways in bacteria for sugar metabolism include the Embden-Meyerhoff-Parnas (EMP) pathway (also known as the glycolytic or fructose biphosphate pathway), the hexosemonophosphate (HMP) pathway (also known as the pentose shunt or pentose phosphate pathway), and the Entner-Doudoroff (ED) pathway (for review, see Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York, and Stryer, L. (1988) Biochemistry, Chapters 13-19, Freeman: New York, and references therein).

The EMP pathway converts hexose molecules to pyruvate, and in the process produces 2 molecules of ATP and 2 molecules of NADH. Starting with glucose-1-phosphate (which may be either directly taken up from the medium, or alternatively may be generated from glycogen, starch, or cellulose), the glucose molecule is isomerized to fructose-6-phosphate, is phosphorylated, and split into two 3-carbon molecules of glyceraldehyde-3-phosphate. After dehydrogenation, phosphorylation, and successive rearrangements, pyruvate results.

The HMP pathway converts glucose to reducing equivalents, such as NADPH, and produces pentose and tetrose compounds which are necessary as intermediates and precursors in a number of other metabolic pathways. In the HMP pathway, glucose-6-phosphate is converted to ribulose-5-phosphate by two successive dehydrogenase reactions (which also release two NADPH molecules), and a carboxylation step. Ribulose-5-phosphate may also be converted to xyulose-5-phosphate and ribose-5-phosphate; the former can undergo a series of biochemical steps to glucose-6-phosphate, which may enter the EMP pathway, while the latter is commonly utilized as an intermediate in other biosynthetic pathways within the cell.

The ED pathway begins with the compound glucose or gluconate, which is subsequently phosphorylated and dehydrated to form 2-dehydro-3-deoxy-6-P-gluconate.

Glucuronate and galacturonate may also be converted to 2-dehydro-3-deoxy-6-P-gluconate through more complex biochemical pathways. This product molecule is subsequently cleaved into glyceraldehyde-3-P and pyruvate; glyceraldehyde-3-P may itself also be converted to pyruvate.

5 The EMP and HMP pathways share many features, including intermediates and enzymes. The EMP pathway provides the greatest amount of ATP, but it does not produce ribose-5-phosphate, an important precursor for, *e.g.*, nucleic acid biosynthesis, nor does it produce erythrose-4-phosphate, which is important for amino acid biosynthesis. Microorganisms that are capable of using only the EMP pathway for
10 glucose utilization are thus not able to grow on simple media with glucose as the sole carbon source. They are referred to as fastidious organisms, and their growth requires inputs of complex organic compounds, such as those found in yeast extract.

In contrast, the HMP pathway produces all of the precursors necessary for both nucleic acid and amino acid biosynthesis, yet yields only half the amount of ATP energy
15 that the EMP pathway does. The HMP pathway also produces NADPH, which may be used for redox reactions in biosynthetic pathways. The HMP pathway does not directly produce pyruvate, however, and thus these microorganisms must also possess this portion of the EMP pathway. It is therefore not surprising that a number of microorganisms, particularly the facultative anaerobes, have evolved such that they
20 possess both of these pathways.

The ED pathway has thus far has only been found in bacteria. Although this pathway is linked partly to the HMP pathway in the reverse direction for precursor formation, the ED pathway directly forms pyruvate by the aldolase cleavage of 3-ketodeoxy-6-phosphogluconate. The ED pathway can exist on its own and is utilized by
25 the majority of strictly aerobic microorganisms. The net result is similar to that of the HMP pathway, although one mole of ATP can be formed only if the carbon atoms are converted into pyruvate, instead of into precursor molecules.

The pyruvate molecules produced through any of these pathways can be readily converted into energy via the Krebs cycle (also known as the citric acid cycle, the citrate
30 cycle, or the tricarboxylic acid cycle (TCA cycle)). In this process, pyruvate is first decarboxylated, resulting in the production of one molecule of NADH, 1 molecule of acetyl-CoA, and 1 molecule of CO₂. The acetyl group of acetyl CoA then reacts with

the 4 carbon unit, oxaloacetate, leading to the formation of citric acid, a 6 carbon organic acid. Dehydration and two additional CO₂ molecules are released. Ultimately, oxaloacetate is regenerated and can serve again as an acetyl acceptor, thus completing the cycle. The electrons released during the oxidation of intermediates in the TCA cycle
5 are transferred to NAD⁺ to yield NADH.

During respiration, the electrons from NADH are transferred to molecular oxygen or other terminal electron acceptors. This process is catalyzed by the respiratory chain, an electron transport system containing both integral membrane proteins and membrane associated proteins. This system serves two basic functions: first, to accept
10 electrons from an electron donor and to transfer them to an electron acceptor, and second, to conserve some of the energy released during electron transfer by the synthesis of ATP. Several types of oxidation-reduction enzymes and electron transport proteins are known to be involved in such processes, including the NADH dehydrogenases, flavin-containing electron carriers, iron sulfur proteins, and cytochromes. The NADH
15 dehydrogenases are located at the cytoplasmic surface of the plasma membrane, and transfer hydrogen atoms from NADH to flavoproteins, in turn accepting electrons from NADH. The flavoproteins are a group of electron carriers possessing a flavin prosthetic group which is alternately reduced and oxidized as it accepts and transfers electrons. Three flavins are known to participate in these reactions: riboflavin, flavin-adenine
20 dinucleotide (FAD) and flavin-mononucleotide (FMN). Iron sulfur proteins contain a cluster of iron and sulfur atoms which are not bonded to a heme group, but which still are able to participate in dehydration and rehydration reactions. Succinate dehydrogenase and aconitase are exemplary iron-sulfur proteins; their iron-sulfur complexes serve to accept and transfer electrons as part of the overall electron-transport
25 chain. The cytochromes are proteins containing an iron porphyrin ring (heme). There are a number of different classes of cytochromes, differing in their reduction potentials. Functionally, these cytochromes form pathways in which electrons may be transferred to other cytochromes having increasingly more positive reduction potentials. A further class of non-protein electron carriers is known: the lipid-soluble quinones (*e.g.*,
30 coenzyme Q). These molecules also serve as hydrogen atom acceptors and electron donors.

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The action of the respiratory chain generates a proton gradient across the cell membrane, resulting in proton motive force. This force is utilized by the cell to synthesize ATP, via the membrane-spanning enzyme, ATP synthase. This enzyme is a multiprotein complex in which the transport of H^+ molecules through the membrane results in the physical rotation of the intracellular subunits and concomitant phosphorylation of ADP to form ATP (for review, see Fillingame, R.H. and Divall, S. (1999) *Novartis Found. Symp.* 221: 218-229, 229-234).

Non-hexose carbon substrates may also serve as carbon and energy sources for cells. Such substrates may first be converted to hexose sugars in the gluconeogenesis pathway, where glucose is first synthesized by the cell and then is degraded to produce energy. The starting material for this reaction is phosphoenolpyruvate (PEP), which is one of the key intermediates in the glycolytic pathway. PEP may be formed from substrates other than sugars, such as acetic acid, or by decarboxylation of oxaloacetate (itself an intermediate in the TCA cycle). By reversing the glycolytic pathway (utilizing a cascade of enzymes different than those of the original glycolysis pathway), glucose-6-phosphate may be formed. The conversion of pyruvate to glucose requires the utilization of 6 high energy phosphate bonds, whereas glycolysis only produces 2 ATP in the conversion of glucose to pyruvate. However, the complete oxidation of glucose (glycolysis, conversion of pyruvate into acetyl CoA, citric acid cycle, and oxidative phosphorylation) yields between 36-38 ATP, so the net loss of high energy phosphate bonds experienced during gluconeogenesis is offset by the overall greater gain in such high-energy molecules produced by the oxidation of glucose.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SMP nucleic acid and protein molecules, which participate in the conversion of sugars to useful degradation products and energy (e.g., ATP) in *C. glutamicum* or which may participate in the production of useful energy-rich molecules (e.g., ATP) by other processes, such as oxidative phosphorylation. In one embodiment, the SMP molecules participate in the metabolism of carbon compounds such as sugars or the generation of energy molecules (e.g., ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In a preferred embodiment,

the activity of the SMP molecules of the present invention to contribute to carbon metabolism or energy production in *C. glutamicum* has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SMP molecules of the invention are modulated in activity, such that the *C. glutamicum*

5 metabolic and energetic pathways in which the SMP proteins of the invention participate are modulated in yield, production, and/or efficiency of production, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "SMP protein" or "SMP polypeptide" includes proteins which are

10 capable of performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Examples of SMP proteins include those encoded by the SMP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SMP gene" or "SMP nucleic acid sequence" include nucleic acid

15 sequences encoding an SMP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SMP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product

20 per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for

25 example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate

30 compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation

products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The term "degradation product" is art-recognized and includes breakdown products of a compound. Such products may themselves have utility as precursor (starting point) or intermediate molecules necessary
5 for the biosynthesis of other compounds by the cell. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

10 In another embodiment, the SMP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum*
15 strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as
20 ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (e.g., by manipulating the genes encoding enzymes involved in the degradation
25 and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (e.g., the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or
30 more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of

reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical. Further, a number of the degradation and intermediate compounds produced during sugar metabolism are necessary precursors and intermediates for other biosynthetic pathways throughout the cell. For example, many amino acids are synthesized directly from compounds normally resulting from glycolysis or the TCA cycle (*e.g.*, serine is synthesized from 3-phosphoglycerate, an intermediate in glycolysis). Thus, by increasing the efficiency of conversion of sugars to useful energy molecules, it is also possible to increase the amount of useful degradation products as well.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* SMP DNAs and the predicted amino acid sequences of the *C. glutamicum* SMP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins having a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention

(e.g., the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

An SMP protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (e.g., ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or can have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SMP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SMP-encoding nucleic acid (e.g., SMP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the

genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SMP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SMP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and

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appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SMP nucleotide sequence can be prepared by standard synthetic techniques, e.g.,
5 using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* SMP DNAs of the invention. This DNA comprises
10 sequences encoding SMP proteins (i.e., the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing.. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in nucleic acid sequences of the
15 Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation "RXA," "RXN," or "RXS" followed by 5 digits (i.e., RXA01626, RXN00043, or RXS0735). Each of the nucleic acid sequences
20 comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, or
25 RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02735 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The
30 sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated

RXA00042 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00042, and the amino acid sequence designated RXN00043 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00043. The correspondence between the RXA, RXN and RXS nucleotide and
5 amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA designation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as
10 "F RXA01312", is an F-designated gene, as are SEQ ID NOs: 29, 33, and 39 (designated on Table 1 as "F RXA02803", "F RXA02854", and "F RXA01365", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence
15 for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

20 In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is
25 sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,
30 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%,

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87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited
5 ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*,
10 hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer
15 or a fragment encoding a biologically active portion of an SMP protein. The nucleotide sequences determined from the cloning of the SMP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SMP homologues in other cell types and organisms, as well as SMP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises
20 substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of
25 one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SMP homologues. Probes based on the SMP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.*
30 the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SMP protein, such as by measuring a level of an SMP-encoding

nucleic acid in a sample of cells, *e.g.*, detecting SMP mRNA levels or determining whether a genomic SMP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently
5 homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. As used
10 herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the
15 protein or portion thereof is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Protein members of such sugar metabolic pathways or energy producing systems, as described herein, may play a role in the production and secretion of one or more fine
20 chemicals. Examples of such activities are also described herein. Thus, "the function of an SMP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SMP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least
25 about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the SMP nucleic acid molecules of the invention
30 are preferably biologically active portions of one of the SMP proteins. As used herein, the term "biologically active portion of an SMP protein" is intended to include a portion, *e.g.*, a domain/motif, of an SMP protein that participates in the metabolism of carbon

compounds such as sugars, or in energy-generating pathways in *C. glutamicum*, or has an activity as set forth in Table 1. To determine whether an SMP protein or a biologically active portion thereof can participate in the metabolism of carbon compounds or in the production of energy-rich molecules in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SMP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SMP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SMP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same SMP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 58% identical to the nucleotide sequence designated RXA00014 (SEQ ID NO:41),

- a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00195 (SEQ ID NO:399), and a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00196 (SEQ ID NO:401). One of ordinary skill in the art would be able to
- 5 calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the
- 10 lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%,
- 15 98%, 99% or more identical) are also encompassed by the invention.

- In addition to the *C. glutamicum* SMP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SMP proteins may exist within a population (*e.g.*, the *C.*
- 20 *glutamicum* population). Such genetic polymorphism in the SMP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SMP protein, preferably a *C. glutamicum* SMP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the
- 25 SMP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SMP that are the result of natural variation and that do not alter the functional activity of SMP proteins are intended to be within the scope of the invention.

- Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SMP DNA of the invention can be isolated based on
- 30 their homology to the *C. glutamicum* SMP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in

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another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or
5 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about
10 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by
15 one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*,
20 encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SMP protein.

In addition to naturally-occurring variants of the SMP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to
25 changes in the amino acid sequence of the encoded SMP protein, without altering the functional ability of the SMP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SMP proteins (*e.g.*, an
30 even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SMP protein, whereas an "essential" amino acid residue is required for SMP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only

semi-conserved in the domain having SMP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SMP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SMP proteins that contain changes in amino acid residues that are not essential
5 for SMP activity. Such SMP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SMP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the
10 invention and is capable of participate in the metabolism of carbon compounds such as sugars, or in the biosynthesis of high-energy compounds in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-
15 70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of
20 the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one
25 sequence (*e.g.*, one of the amino acid sequences the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two
30 sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SMP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that

5 one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid

10 substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine,

15 threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SMP protein is preferably replaced with another amino acid residue from the same

20 side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SMP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SMP activity described herein to identify mutants that retain SMP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing,

25 the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SMP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which

30 are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or

complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SMP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SMP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of NO. 3 (RXA01626) comprises nucleotides 1 to 345). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SMP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SMP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SMP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SMP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SMP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-

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galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-
5 methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense
10 nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered
15 to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SMP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through
20 specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve
25 sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms
30 specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-

methyribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are
5 capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SMP mRNA transcripts to thereby inhibit translation of SMP mRNA. A ribozyme having specificity for an SMP-encoding nucleic acid can be
10 designed based upon the nucleotide sequence of an SMP cDNA disclosed herein (*i.e.*, SEQ ID NO. 3 (RXA01626)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SMP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No.
15 5,116,742. Alternatively, SMP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, SMP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SMP nucleotide sequence (*e.g.*,
20 an SMP promoter and/or enhancers) to form triple helical structures that prevent transcription of an SMP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

25 B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SMP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid",
30 which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of

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autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector.

10 However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells.

Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *amy*, *SPO2*, λ -*P_R*- or λ *P_L*, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MF α* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*,

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usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors
5 of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., SMP proteins, mutant forms of SMP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SMP proteins in prokaryotic or eukaryotic cells. For example, SMP genes
10 can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer
15 systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis*
20 *thaliana* leaf and cotyledon explants" *Plant Cell Rep*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

25 Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors
30 typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion

expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

5 Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SMP protein is cloned into a
10 pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SMP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

15 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
20 Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by
25 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
30 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another
5 strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

10 In another embodiment, the SMP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and
15 methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier:
20 New York (ISBN 0 444 904018).

Alternatively, the SMP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989)
25 *Virology* 170:31-39).

In another embodiment, the SMP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New
30 plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+,

pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.*

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in

a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SMP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SMP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

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transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SMP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SMP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SMP gene. Preferably, this SMP gene is a *Corynebacterium glutamicum* SMP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SMP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SMP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SMP protein). In the homologous recombination vector, the altered portion of the SMP gene is flanked at its 5' and 3' ends by additional nucleic acid of the SMP gene to allow for homologous recombination to occur between the exogenous SMP gene carried by the vector and an endogenous SMP gene in a microorganism. The additional

flanking SMP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination
5 vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SMP gene has homologously recombined with the endogenous SMP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.
10 For example, inclusion of an SMP gene on a vector placing it under control of the lac operon permits expression of the SMP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SMP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that
15 expression of its protein product does not occur. In another embodiment, an endogenous or introduced SMP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion,
20 truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SMP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

25 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SMP protein. Accordingly, the invention further provides methods for producing SMP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SMP protein has
30 been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SMP protein) in a suitable medium until SMP protein is produced. In another

embodiment, the method further comprises isolating SMP proteins from the medium or the host cell.

C. Isolated SMP Proteins

5 Another aspect of the invention pertains to isolated SMP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes
10 preparations of SMP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SMP protein having less than about 30% (by dry weight) of non-SMP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SMP protein,
15 still more preferably less than about 10% of non-SMP protein, and most preferably less than about 5% non-SMP protein. When the SMP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein
20 preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein having less than about 30% (by
25 dry weight) of chemical precursors or non-SMP chemicals, more preferably less than about 20% chemical precursors or non-SMP chemicals, still more preferably less than about 10% chemical precursors or non-SMP chemicals, and most preferably less than about 5% chemical precursors or non-SMP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from
30 the same organism from which the SMP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SMP protein in a microorganism such as *C. glutamicum*.

An isolated SMP protein or a portion thereof of the invention can participate in the metabolism of carbon compounds such as sugars, or in the production of energy compounds (e.g., by oxidative phosphorylation) utilized to drive unfavorable metabolic pathways, or has one or more of the activities set forth in Table 1. In preferred

5 embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as

10 oxidative phosphorylation in *Corynebacterium glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SMP protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a

15 nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of the invention (e.g., a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least

20 about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity

25 values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described

30 herein. For example, a preferred SMP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of the invention, and

which can perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or which has one or more of the activities set forth in Table 1.

5 In other embodiments, the SMP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in
10 another embodiment, the SMP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or
15 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the SMP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of
20 identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

 Biologically active portions of an SMP protein include peptides comprising
25 amino acid sequences derived from the amino acid sequence of an SMP protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an SMP protein, which include fewer amino acids than a full length SMP protein or the full length protein which is homologous to an SMP protein, and exhibit at least one activity of an SMP protein.
30 Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SMP protein. Moreover, other

biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SMP protein include one or more selected domains/motifs or portions thereof having biological activity.

5 SMP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SMP protein is expressed in the host cell. The SMP protein can then be isolated from the cells by an appropriate purification scheme using standard
10 protein purification techniques. Alternative to recombinant expression, an SMP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SMP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SMP antibody, which can be produced by standard techniques utilizing an SMP protein or fragment thereof of this invention.

15 The invention also provides SMP chimeric or fusion proteins. As used herein, an SMP "chimeric protein" or "fusion protein" comprises an SMP polypeptide operatively linked to a non-SMP polypeptide. An "SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an SMP protein, whereas a "non-SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a
20 protein which is not substantially homologous to the SMP protein, *e.g.*, a protein which is different from the SMP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SMP polypeptide and the non-SMP polypeptide are fused in-frame to each other. The non-SMP polypeptide can be fused to the N-terminus or C-terminus of
25 the SMP polypeptide. For example, in one embodiment the fusion protein is a GST-SMP fusion protein in which the SMP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SMP proteins. In another embodiment, the fusion protein is an SMP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian
30 host cells), expression and/or secretion of an SMP protein can be increased through use of a heterologous signal sequence.

Preferably, an SMP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended
5 termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide).
15 An SMP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SMP protein.

Homologues of the SMP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the SMP protein. As used herein, the term "homologue" refers to a variant form of the SMP protein which acts as an agonist or antagonist of the
20 activity of the SMP protein. An agonist of the SMP protein can retain substantially the same, or a subset, of the biological activities of the SMP protein. An antagonist of the SMP protein can inhibit one or more of the activities of the naturally occurring form of the SMP protein, by, for example, competitively binding to a downstream or upstream member of the sugar molecule metabolic cascade or the energy-producing pathway
25 which includes the SMP protein.

In an alternative embodiment, homologues of the SMP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SMP protein for SMP protein agonist or antagonist activity. In one embodiment, a variegated library of SMP variants is generated by combinatorial mutagenesis at the nucleic acid
30 level and is encoded by a variegated gene library. A variegated library of SMP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SMP

sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SMP sequences therein. There are a variety of methods which can be used to produce libraries of potential SMP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a
5 degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SMP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3;
10 Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SMP protein coding can be used to generate a variegated population of SMP fragments for screening and subsequent selection of homologues of an SMP protein. In one embodiment, a library of coding
15 sequence fragments can be generated by treating a double stranded PCR fragment of an SMP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by
20 treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SMP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA
25 libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SMP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of
30 vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the

frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SMP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a
5 variegated SMP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the
10 following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SMP protein regions required for function; modulation of an SMP protein activity; modulation of the metabolism of one or more sugars; modulation of high-energy molecule production in a
15 cell (*i.e.*, ATP, NADPH); and modulation of cellular production of a desired compound, such as a fine chemical.

The SMP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum*
20 or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.
25 Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli
30 secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and

spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

- 5 In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of
- 10 *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

- The nucleic acid and protein molecules of the invention may also serve as
- 15 markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed
- 20 with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the
- 25 invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

- The SMP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and energy-releasing processes in which
- 30 the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the

evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein
5 engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the SMP nucleic acid molecules of the invention may result in the production of SMP proteins having functional differences from the wild-type SMP proteins. These proteins may be improved in efficiency or activity, may be present in
10 greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention. In such methods, a microorganism
15 expressing one or more SMP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SMP protein is assessed.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production
20 of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar
25 compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the
30 genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit

unfavorable, yet desired metabolic reactions (e.g., the biosynthesis of a desired fine chemical) to occur.

Further, modulation of one or more pathways involved in sugar utilization permits optimization of the conversion of the energy contained within the sugar molecule to the production of one or more desired fine chemicals. For example, by reducing the activity of enzymes involved in, for example, gluconeogenesis, more ATP is available to drive desired biochemical reactions (such as fine chemical biosyntheses) in the cell. Also, the overall production of energy molecules from sugars may be modulated to ensure that the cell maximizes its energy production from each sugar molecule. Inefficient sugar utilization can lead to excess CO₂ production and excess energy, which may result in futile metabolic cycles. By improving the metabolism of sugar molecules, the cell should be able to function more efficiently, with a need for fewer carbon molecules. This should result in an improved fine chemical product: sugar molecule ratio (improved carbon yield), and permits a decrease in the amount of sugars that must be added to the medium in large-scale fermentor culture of such engineered *C. glutamicum*.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (e.g., by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (e.g., nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical.

Further, many of the degradation products produced during sugar metabolism are themselves utilized by the cell as precursors or intermediates for the production of a number of other useful compounds, some of which are fine chemicals. For example, pyruvate is converted into the amino acid alanine, and ribose-5-phosphate is an integral part of, for example, nucleotide molecules. The amount and efficiency of sugar metabolism, then, has a profound effect on the availability of these degradation products in the cell. By increasing the ability of the cell to process sugars, either in terms of efficiency of existing pathways (*e.g.*, by engineering enzymes involved in these pathways such that they are optimized in activity), or by increasing the availability of the enzymes involved in such pathways (*e.g.*, by increasing the number of these enzymes present in the cell), it is possible to also increase the availability of these degradation products in the cell, which should in turn increase the production of many different other desirable compounds in the cell (*e.g.*, fine chemicals).

The aforementioned mutagenesis strategies for SMP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SMP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: GENES IN THE APPLICATION

HMP:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXS02735	VV0074	14576	15280	6-Phosphoglucolactonase
3	4	RXA01626	GR00452	4270	3926	L-ribulose-phosphate 4-epimerase
5	6	RXA02245	GR00654	13639	14295	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
7	8	RXA01015	GR00290	346	5	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6)

TCA:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
9	10	RXN01312	VV0082	20803	18785	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
11	12	F RXA01312	GR00380	2690	1614	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
13	14	RXN00231	VV0083	15484	14015	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1.2.1.16)
15	16	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
17	18	RXA01535	GR00427	1354	2760	FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2)
19	20	RXA00517	GR00131	1407	2447	MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82)
21	22	RXA01350	GR00392	1844	2827	MALATE DEHYDROGENASE (EC 1.1.1.37)

EMB-Pathway

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
23	24	RXA02149	GR00639	17786	18754	GLUCOKINASE (EC 2.7.1.2)
25	26	RXA01814	GR00515	2571	910	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
27	28	RXN02803	VV0086	1	657	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
29	30	F RXA02803	GR00784	2	400	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
31	32	RXN03076	VV0043	1624	35	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
33	34	F RXA02854	GR10002	1588	5	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
35	36	RXA00511	GR00129	1	513	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
37	38	RXN01365	VV0091	1476	103	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
39	40	F RXA01365	GR00397	897	4	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
41	42	RXA00098	GR00014	6525	8144	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9)
43	44	RXA01989	GR00578	1	630	GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9)
45	46	RXA00340	GR00059	1549	2694	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
47	48	RXA02492	GR00720	2201	2917	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
49	50	RXA00381	GR00082	1451	846	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
51	52	RXA02122	GR00636	6511	5813	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
53	54	RXA00206	GR00032	6171	5134	6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11)
55	56	RXA01243	GR00359	2302	3261	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
57	58	RXA01882	GR00538	1165	2154	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
59	60	RXA01702	GR00479	1397	366	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13)
61	62	RXA02258	GR00654	26451	27227	TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1)
63	64	RXN01225	VV0064	6382	4943	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
65	66	F RXA01225	GR00354	5302	6741	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE HOMOLOG
67	68	RXA02256	GR00654	23934	24935	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
69	70	RXA02257	GR00654	25155	26369	PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)
71	72	RXA00235	GR00036	2365	1091	ENOLASE (EC 4.2.1.11)
73	74	RXA01093	GR00306	1552	122	PYRUVATE KINASE (EC 2.7.1.40)
75	76	RXN02675	VV0098	72801	70945	PYRUVATE KINASE (EC 2.7.1.40)
77	78	F RXA02675	GR00754	2	364	PYRUVATE KINASE (EC 2.7.1.40)
79	80	F RXA02695	GR00755	2949	4370	PYRUVATE KINASE (EC 2.7.1.40)
81	82	RXA00682	GR00179	5299	3401	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
83	84	RXA00683	GR00179	6440	5349	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
85	86	RXN00635	VV0135	22708	20972	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
87	88	F RXA02807	GR00788	88	552	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
89	90	F RXA00635	GR00167	3	923	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
91	92	RXN03044	VV0019	1391	2221	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
93	94	F RXA02852	GR00852	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
95	96	F RXA00268	GR00041	125	955	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
97	98	RXN03086	VV0049	2243	2650	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
99	100	F RXA02887	GR10022	411	4	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
101	102	RXN03043	VV0019	1	1362	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
103	104	F RXA02897	GR10039	1291	5	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
105	106	RXN03083	VV0047	88	1110	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
107	108	F RXA02853	GR10001	89	1495	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
109	110	RXA02259	GR00654	27401	30172	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
111	112	RXN02326	VV0047	4500	5315	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
113	114	F RXA02326	GR00668	5338	4523	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
115	116	RXN02327	VV0047	3533	4492	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
117	118	F RXA02327	GR00668	6305	5346	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
119	120	RXN02328	VV0047	1842	3437	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
121	122	F RXA02328	GR00668	7783	6401	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
123	124	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
125						
126		F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
127		F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
128		RXA02694	GR00755	1879	2820	L-LACTATE DEHYDROGENASE (EC 1.1.1.27)
129		RXA00296	VW01176	35763	38606	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
130		RXA00296	GR00048	3	2837	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
131		RXA01901	GR00544	4158	5417	L-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.3)
132		RXA01952	VW0105	9954	11666	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
133		RXA01952	GR00562	1	216	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
134		RXA01955	GR00562	4611	6209	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
135		RXA01955	GR00047	2645	1734	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
136		RXA01130	VW0157	6138	5536	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
137		RXA01130	GR00315	2	304	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
138		RXA01130	VW0085	509	6	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
139		RXA01133	GR00316	568	1116	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
140		RXA01133	VW0127	3127	2240	IOLB PROTEIN
141		RXA00871	GR00239	2344	3207	IOLB PROTEIN: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D- GLYCERALDEHYDE 3-PHOSPHATE.
142						
143						
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153						
154						
155						
156						
157		RXN02829	VW0354	287	559	IOLS PROTEIN
158		RXN02829	GR00816	287	562	IOLS PROTEIN
159		RXN02829	VW0019	7474	8298	NAGD PROTEIN
160		RXN01468	GR00422	1250	2074	PUTATIVE N-GLYCERALDEHYDE-2-PHOSPHOTRANSFERASE
161		RXN01468	GR00211	3993	2989	GLPX PROTEIN
162		RXN01468	VW0213	6135	5224	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
163		RXN01468	GR00290	1390	686	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
164		RXN01468	VW0098	59053	58385	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
165		RXN01468	VW0052	3216	3428	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
166		RXN01468	VW0377	310	519	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
167		RXN01468	VW0382	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
168		RXN01468	VW0098	14370	12541	PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
169		RXN01468	VW0009	3477	2296	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
170						
171						
172						
173						
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183		RXS01261	VW0009	3703	3533	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

Glycerol metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
185						
186		RXA02640	GR00749	1400	2926	GLYCEROL KINASE (EC 2.7.1.30)
187		RXA01025	VW0143	5483	4488	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P) ⁺) (EC 1.1.1.94)
188		RXA01025	GR00293	939	1853	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P) ⁺) (EC 1.1.1.94)
189		RXA01025	GR00525	3515	1830	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.1.94)
190		RXA01851	GR00359	1526	2302	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
191		RXA01242	GR00661	992	147	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
192						
193						
194						
195						

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
197	198	RXN01891	VW0122	24949	24086	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
199	200	F RXA01891	GR00541	1736	918	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
201	202	RXA02414	GR00703	3808	3062	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
203	204	RXN01580	VW0122	22091	22807	Glycerophosphoryl diester phosphodiesterase

Acetate metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
205	206	RXA01436	GR00418	2547	1357	ACETATE KINASE (EC 2.7.2.1)
207	208	RXA00686	GR00179	8744	7941	ACETATE OPERON REPRESSOR
209	210	RXA00246	GR00037	4425	3391	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
211	212	RXA01571	GR00438	1360	1959	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
213	214	RXA01572	GR00438	1928	2419	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
215	216	RXA01758	GR00498	3961	2945	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
217	218	RXA02539	GR00726	11676	10159	ALDEHYDE DEHYDROGENASE (EC 1.1.1.1)
219	220	RXN03061	VW0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
221	222	RXN03150	VW0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
223	224	RXN01340	VW0033	3	860	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
225	226	RXN01498	VW0008	1598	3160	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
227	228	RXN02674	VW0315	15614	14163	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
229	230	RXN00868	VW0127	2230	320	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
231	232	RXN01143	VW0077	9372	8254	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
233	234	RXN01146	VW0264	243	935	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
235	236	RXN01144	VW0077	8237	7722	ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)

Butanediol, diacetyl and acetoin formation

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
237	238	RXA02474	GR00715	8082	7309	(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76)
239	240	RXA02453	GR00710	6103	5351	ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5)
241	242	RXS01758	VW0112	27383	28399	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

Table 1 (continued)

HMP-Cycle

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
243	244	RXA02737	GR00763	3312	1771	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49)
245	246	RXA02738	GR00763	4499	3420	TRANSALDOLASE (EC 2.2.1.2)
247	248	RXA02739	GR00763	6769	4670	TRANSKETOLASE (EC 2.2.1.1)
249	250	RXA00965	GR00270	1232	510	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
251	252	RXN00999	VV0106	2817	1366	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
253	254	F RXA00999	GR00283	3012	4448	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)

Nucleotide sugar conversion

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
255	256	RXN02596	VV0098	48784	47582	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
257	258	F RXA02596	GR00742	1	489	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
259	260	F RXA02642	GR00749	5383	5880	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
261	262	RXA02572	GR00737	2	646	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
263	264	RXA02485	GR00718	2345	3445	UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
265	266	RXA01216	GR00352	2302	1202	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23)
267	268	RXA01259	GR00367	987	130	UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9)
269	270	RXA02028	GR00616	573	998	UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9)
271	272	RXA01262	GR00367	8351	7191	GDP-MANNOSE 6-DEHYDROGENASE (EC 1.1.1.132)
273	274	RXA01377	GR00400	3935	5020	MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13)
275	276	RXA02063	GR00626	3301	4527	GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (EC 2.7.7.27)
277	278	RXN00014	VV0048	8848	9627	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
279	280	F RXA00014	GR00002	4448	5227	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
281	282	RXA01570	GR00438	427	1281	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
283	284	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40)
285	286	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)

Inositol and ribitol metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
287	288	RXA01887	GR00539	4219	3209	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
289	290	RXN00013	VW0048	7966	8838	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
291	292	F RXA00013	GR00002	3566	4438	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
293	294	RXA01099	GR00306	6328	5504	INOSITOL MONOPHOSPHATE PHOSPHATASE
295	296	RXN01332	VW0273	579	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
297	298	F RXA01332	GR00388	552	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
299	300	RXA01632	GR00454	2338	3342	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
301	302	RXA01633	GR00454	3380	4462	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
303	304	RXN01406	VW0278	2999	1977	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
305	306	RXN01630	VW0050	48113	47037	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
307	308	RXN00528	VW0079	23406	22318	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4)
309	310	RXN03057	VW0028	7017	7688	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
311	312	F RXA02902	GR10040	10277	10948	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
313	314	RXA00251	GR00038	931	224	RIBITOL 2-DEHYDROGENASE (EC 1.1.1.56)

Utilization of sugars

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
315	316	RXN02654	VW0090	12206	13090	GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47)
317	318	F RXA02654	GR00752	7405	8289	GLUCOSE 1-DEHYDROGENASE II (EC 1.1.1.47)
319	320	RXN01049	VW0079	9633	11114	GLUCONOKINASE (EC 2.7.1.12)
321	322	F RXA01049	GR00296	1502	492	GLUCONOKINASE (EC 2.7.1.12)
323	324	F RXA01050	GR00296	1972	1499	GLUCONOKINASE (EC 2.7.1.12)
325	326	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
327	328	RXN00872	VW0127	6557	5604	FRUCTOKINASE (EC 2.7.1.4)
329	330	F RXA00872	GR00240	565	1086	FRUCTOKINASE (EC 2.7.1.4)
331	332	RXN00799	VW0009	58477	56834	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
333	334	F RXA00799	GR00214	1	1584	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
335	336	RXA00032	GR00003	12028	10520	MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67)
337	338	RXA02528	GR00725	6880	7854	FRUCTOSE REPRESSOR
339	340	RXN00316	VW0006	7035	8180	Hypothetical Oxidoreductase (EC 1.1.1.-)
341	342	F RXA00309	GR00053	316	5	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
343	344	RXN00310	VW0006	6616	7050	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
345	346	F RXA00310	GR00053	735	301	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
347	348	RXA00041	GR00007	1246	5	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
349	350	RXA02026	GR00615	725	6	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
351	352	RXA02061	GR00626	1842	349	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
353	354	RXN01369	VV0124	595	1776	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
355	356	F RXA01369	GR00398	3	503	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
357	358	F RXA01373	GR00399	595	1302	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
359	360	RXA02611	GR00743	1	1752	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
361	362	RXA02612	GR00743	1793	3985	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
363	364	RXN01884	VV0184	1	1890	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25)
365	366	F RXA01884	GR00539	3	1475	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25)
367	368	RXA01111	GR00306	16981	17427	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25)
370	370	RXN01550	VV0143	14749	16260	GLYCOGEN OPERON PROTEIN GLX (EC 3.2.1.-)
371	372	F RXA01550	GR00431	3	1346	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
373	374	RXN02100	VV0318	2	2326	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
375	376	F RXA02100	GR00631	3	920	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
377	378	F RXA02113	GR00633	2	1207	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
379	380	RXA02147	GR00639	15516	16532	ALPHA-AMYLASE (EC 3.2.1.1)
381	382	RXA01478	GR00422	10517	12352	GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.2.1.3)
383	384	RXA01888	GR00539	4366	4923	GLUCOSE-RESISTANCE AMYLASE REGULATOR
385	386	RXN01927	VV0127	50623	49244	XYLULOSE KINASE (EC 2.7.1.17)
387	388	F RXA01927	GR00555	3	1118	XYLULOSE KINASE (EC 2.7.1.17)
389	390	RXA02729	GR00762	747	4	RIBOKINASE (EC 2.7.1.15)
391	392	RXA02797	GR00778	1739	2641	RIBOKINASE (EC 2.7.1.15)
393	394	RXA02730	GR00762	1768	731	RIBOSE OPERON REPRESSOR
395	396	RXA02551	GR00729	2193	2552	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86)
397	398	RXA01325	GR00385	5676	5005	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)
399	400	RXA00195	GR00030	543	1103	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
401	402	RXA00196	GR00030	1094	1708	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
403	404	RXN01562	VV0191	1230	3137	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
405	406	F RXA01562	GR00436	2	1039	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
407	408	F RXA01705	GR00480	971	1573	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
409	410	RXN00879	VV0099	8763	6646	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25)
411	412	F RXA00879	GR00242	5927	3828	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25)
413	414	RXN00043	VV0119	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
415	416	F RXA00043	GR00007	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
417	418	RXN01752	VV0127	35265	33805	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
419	420	F RXA01839	GR00520	1157	510	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
421	422	RXA01859	GR00529	1473	547	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
423	424	RXA00042	GR00007	2037	1279	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
425	426	RXA01482	GR00422	17271	15397	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)
427	428	RXN03179	VV0336	2	667	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)
429	430	F RXA02872	GR10013	675	4	(ISOMERIZING) (EC 2.6.1.16)
431	432	RXN03180	VV0337	672	163	URONATE ISOMERASE (EC 5.3.1.12)
433	434	F RXA02873	GR10014	672	163	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
435	436	RXA02292	GR00662	1611	2285	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
437	438	RXA02666	GR00753	7260	6493	GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3.1.18)
439	440	RXA00202	GR00032	1216	275	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40)
441	442	RXA02440	GR00709	5097	4258	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
443	444	RXN01569	VW0009	41086	42444	dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
445	446	F RXA01569	GR00438	2	427	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
447	448	F RXA02055	GR00624	7122	8042	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
449	450	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
451	452	RXA02054	GR00624	6103	7119	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
453	454	RXN00427	VW0112	7004	6219	dTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---)
455	456	F RXA00427	GR00098	1591	2022	DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---)
457	458	RXA00327	GR00057	10253	9880	PROTEIN ARAJ
459	460	RXA00328	GR00057	11147	10656	PROTEIN ARAJ
461	462	RXA00329	GR00057	12390	11167	PROTEIN ARAJ
463	464	RXN01554	VW0135	28686	26545	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39)
465	466	RXN03015	VW0063	289	8	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
467	468	RXN03056	VW0028	6258	6935	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
469	470	RXN03030	VW0009	57006	56443	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
471	472	RXN00401	VW0025	12427	11489	5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41)
473	474	RXN02125	VW0102	23242	22442	ALDOSE REDUCTASE (EC 1.1.1.21)
475	476	RXN00200	VW0181	1679	5116	arabinosyl transferase subunit B (EC 2.4.2.-)
477	478	RXN01175	VW0017	39688	38303	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
479	480	RXN01376	VW0091	5610	4750	PUTATIVE GLYCOSYL TRANSFERASE WBIF
481	482	RXN01631	VW0050	47021	46143	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
483	484	RXN01593	VW0229	13274	12408	NAGD PROTEIN
485	486	RXN00337	VW0197	20369	21418	GALACTOKINASE (EC 2.7.1.6)
487	488	RXS00584	VW0323	5516	6640	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
489	490	RXS02574				BETA-HEXOSAMINIDASE A PRECURSOR (EC 3.2.1.52)
491	492	RXS03215				GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
493	494	F RXA01915	GR00549	1	1008	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
495	496	RXS03224				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
497	498	F RXA00038				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
499	500	RXC00233	GR00006	1417	260	protein involved in sugar metabolism
501	502	RXC00236				Membrane Lipoprotein involved in sugar metabolism
503	504	RXC00271				Exported Protein involved in ribose metabolism
505	506	RXC00338				protein involved in sugar metabolism
507	508	RXC00362				Membrane Spanning Protein involved in metabolism of diols
509	510	RXC00412				Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism
511	512	RXC00526				ABC Transporter ATP-Binding Protein involved in sugar metabolism
513	514	RXC01004				Membrane Spanning Protein involved in sugar metabolism
515	516	RXC01017				Cytosolic Protein involved in sugar metabolism
517	518	RXC01021				Cytosolic Kinase involved in metabolism of sugars and thiamin
519	520	RXC01212				ABC Transporter ATP-Binding Protein involved in sugar metabolism
521	522	RXC01306				Membrane Spanning Protein involved in sugar metabolism
523	524	RXC01366				Cytosolic Protein involved in sugar metabolism
525	526	RXC01372				Cytosolic Protein involved in sugar metabolism

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
527	528	RXC01659				protein involved in sugar metabolism
529	530	RXC01663				protein involved in sugar metabolism
531	532	RXC01693				protein involved in sugar metabolism
533	534	RXC01703				Cytosolic Protein involved in sugar metabolism
535	536	RXC02254				Membrane Associated Protein involved in sugar metabolism
537	538	RXC02255				Cytosolic Protein involved in sugar metabolism
539	540	RXC02435				protein involved in sugar metabolism
541	542	F RXA02435	GR00709	825	268	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
543	544	RXC03216				protein involved in sugar metabolism
TCA-cycle						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
545	546	RXA02175	GR00641	10710	9418	CITRATE SYNTHASE (EC 4.1.3.7)
547	548	RXA02621	GR00746	2647	1829	CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
549	550	RXN00519	VW0144	5585	3372	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
551	552	F RXA00521	GR00133	2	1060	ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42)
553	554	RXN02209	VW0304	1	1671	ACONITATE HYDRATASE (EC 4.2.1.3)
555	556	F RXA02209	GR00648	3	1661	ACONITATE HYDRATASE (EC 4.2.1.3)
557	558	RXN02213	VW0305	1378	2151	ACONITATE HYDRATASE (EC 4.2.1.3)
559	560	F RXA02213	GR00649	1330	2046	ACONITATE HYDRATASE (EC 4.2.1.3)
561	562	RXA02056	GR00625	3	2870	ACONITATE HYDRATASE (EC 4.2.1.3)
563	564	RXA01745	GR00495	2	1495	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2)
565	566	RXA00782	GR00206	3984	3103	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPLEX (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
567	568	RXA00783	GR00206	5280	4009	SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5)
569	570	RXN01695	VW0139	11307	12806	SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5)
571	572	F RXA01615	GR00449	8608	9546	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
573	574	F RXA01695	GR00474	4388	4179	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
575	576	RXA00290	GR00046	4893	5655	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
577	578	RXN01048	VW0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)
579	580	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
581	582	F RXA00290	GR00046	4893	5655	MALIC ENZYME (EC 1.1.1.39)
583	584	RXN03101	VW0066	2	583	MALIC ENZYME (EC 1.1.1.39)
585	586	RXN02046	VW0025	15056	14640	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
587	588	RXN00369	VW0025	11481	9922	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61) oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)

Table 1 (continued)

Glyoxylate bypass

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
589	590	RXN02399	VV0176	19708	18365	ISOCITRATE LYASE (EC 4.1.3.1)
591	592	F RXA02399	GR00699	478	1773	ISOCITRATE LYASE (EC 4.1.3.1)
593	594	RXN02404	VV0176	20259	22475	MALATE SYNTHASE (EC 4.1.3.2)
595	596	F RXA02404	GR00700	3798	1663	MALATE SYNTHASE (EC 4.1.3.2)
597	598	RXA01089	GR00304	3209	3958	GLYOXYLATE-INDUCED PROTEIN
599	600	RXA01886	GR00539	3203	2430	GLYOXYLATE-INDUCED PROTEIN

Methylcitrate-pathway

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
600	602	RXN03117	VV0092	3087	1576	2-methylisocitrate synthase (EC 5.3.3.-)
601	604	F RXA00406	GR00090	978	4	2-methylisocitrate synthase (EC 5.3.3.-)
603	606	F RXA00514	GR00130	1983	1576	2-methylisocitrate synthase (EC 5.3.3.-)
605	608	RXA00512	GR00130	621	4	2-methylcitrate synthase (EC 4.1.3.31)
607	610	RXA00518	GR00131	3069	2773	2-methylcitrate synthase (EC 4.1.3.31)
609	612	RXA01077	GR00300	4647	6017	2-methylisocitrate synthase (EC 5.3.3.-)
611	614	RXN03144	VV0141	2	901	2-methylisocitrate synthase (EC 5.3.3.-)
613	616	F RXA02322	GR00668	415	5	2-methylisocitrate synthase (EC 5.3.3.-)
615	618	RXA02329	GR00669	607	5	2-methylisocitrate synthase (EC 5.3.3.-)
617	620	RXA02332	GR00671	1906	764	2-methylcitrate synthase (EC 4.1.3.31)
619	622	RXN02333	VV0141	901	1815	methylisocitrate lyase (EC 4.1.3.30)
621	624	F RXA02333	GR00671	2120	1902	methylisocitrate lyase (EC 4.1.3.30)
623	626	RXA00030	GR00003	9590	9979	LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)

Methyl-Malonyl-CoA-Mutases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
625	628	RXN00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
627	630	F RXA00148	GR00023	2002	5	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
629	632	RXA00149	GR00023	3856	2009	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)

Table 1 (continued)

Others

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
631	634	RXN00317	VV0197	26879	27532	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
635	636	F RXA00317	GR00055	344	6	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
637	638	RXA02196	GR00645	3956	3264	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
639	640	RXN02461	VV0124	14236	14643	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
641	642	RXN01744	VV0174	2350	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
643	644	F RXA00055	GR00008	11753	11890	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
645	646	F RXA01744	GR00494	2113	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
647	648	RXA00379	GR00082	212	6	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
649	650	RXA00385	GR00083	773	435	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
651	652	RXA01743	GR00494	806	6	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-)
653	654	RXN02480	VV0084	31222	29567	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
655	656	F RXA01919	GR00550	288	4	CYTOCHROME C OXIDASE SUBUNIT I (EC 1.9.3.1)
657	658	F RXA02480	GR00717	1449	601	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
659	660	F RXA02481	GR00717	1945	1334	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
661	662	RXA02140	GR00639	7339	8415	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
663	664	RXA02142	GR00639	9413	10063	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)
665	666	RXA02144	GR00639	11025	12248	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
667	668	RXA02740	GR00763	7613	8542	RIESKE IRON-SULFUR PROTEIN
669	670	RXA02743	GR00763	13534	12497	PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR
671	672	RXA01227	GR00355	1199	1519	CYTOCHROME A3 CONTROLLING PROTEIN
673	674	RXA01865	GR00532	436	122	FERREDOXIN
675	676	RXA00680	GR00179	2632	2315	FERREDOXIN VI
677	678	RXA00679	GR00179	2302	1037	FERREDOXIN--NAD(+) REDUCTASE (EC 1.18.1.3)
679	680	RXA00224	GR00032	24965	24015	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT
681	682	RXA00225	GR00032	25783	24998	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT
683	684	RXN00606	VV0192	11299	9026	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
685	686	F RXA00606	GR00160	121	1869	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
687	688	RXN00595	VV0192	8642	7113	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
689	690	F RXA00608	GR00160	2253	3017	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
691	692	RXA00913	GR00249	3	2120	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
693	694	RXA00909	GR00247	2552	3406	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
695	696	RXA00700	GR00182	846	43	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2
697	698	RXN00483	VV0086	44824	46287	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)

Redox Chain

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
699	700	F RXA00483	GR00119	19106	20569	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)
701	702	RXA01534	GR00427	1035	547	NADH-DEPENDENT FMN OXYDOREDUCTASE
703	704	RXA00288	GR00046	2846	1636	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
705	706	RXA02741	GR00763	9585	8620	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
707	708	RXN02560	VV0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
709	710	F RXA02560	GR00731	6339	7160	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
711	712	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
713	714	RXN03014	GR00358	1273	368	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
715	716	F RXA00910	GR00248	3	1259	Hydrogenase subunits
717	718	RXN01895	VV0117	955	5	NADH DEHYDROGENASE (EC 1.6.99.3)
719	720	F RXA01895	GR00543	2	817	DEHYDROGENASE
721	722	RXA00703	GR00183	2556	271	FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1.2.1.2)
723	724	RXN00705	VV0005	6111	5197	FDHD PROTEIN
725	726	F RXA00705	GR00184	1291	407	FDHD PROTEIN
727	728	RXN00388	VV0025	2081	3091	CYTOCHROME C BIOGENESIS PROTEIN CCSA
729	730	F RXA00388	GR00085	969	667	essential protein similar to cytochrome c
731	732	F RXA00386	GR00084	514	5	RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein
733	734	RXA00945	GR00259	1876	2847	putative cytochrome oxidase
735	736	RXN02556	VV0101	5602	6759	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
737	738	F RXA02556	GR00731	2019	3176	FLAVOHEMOPROTEIN
739	740	RXA01392	GR00408	2297	3373	GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18)
741	742	RXA00800	GR00214	2031	3134	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1)
743	744	RXA02143	GR00639	10138	11025	QCRC PROTEIN, menaquinol:cytochrome c oxidoreductase
745	746	RXN03096	VV0058	405	4	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
747	748	RXN02036	VV0176	32683	33063	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
749	750	RXN02765	VV0317	3552	2784	Hypothetical Oxidoreductase
751	752	RXN02206	VV0302	1784	849	Hypothetical Oxidoreductase
753	754	RXN02554	VV0101	4633	4010	Hypothetical Oxidoreductase (EC 1.1.1.-)

ATP-Synthase

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
755	756	RXN01204	VV0121	1270	461	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
757	758	F RXA01204	GR00345	394	1155	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
759	760	RXA01201	GR00344	675	2315	ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34)
761	762	RXN01193	VV0175	5280	3832	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
763	764	F RXA01193	GR00343	15	755	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
765	766	F RXA01203	GR00344	3355	3993	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
767	768	RXN02821	VW0121	324	85	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
769	770	F RXA02821	GR00802	139	318	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
771	772	RXA01200	GR00344	2	610	ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34)
773	774	RXA01194	GR00343	770	1141	ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)
775	776	RXA01202	GR00344	2375	3349	ATP SYNTHASE GAMMA CHAIN (EC 3.6.1.34)
777	778	RXN02434	VW0090	4923	3274	ATP-BINDING PROTEIN

Cytochrome metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
779	780	RXN00684	VW0005	29864	28581	CYTOCHROME P450 116 (EC 1.14.-.-)
781	782	RXN00387	VW0025	1150	2004	Hypothetical Cytochrome c Biogenesis Protein

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF038651			
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of <i>Corynebacterium glutamicum</i> 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isolation and synthesis in <i>Corynebacterium glutamicum</i> : molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the <i>Corynebacterium glutamicum</i> mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diphtheriae</i> dtxR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranelate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; bmQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rosol, I. et al. "The <i>Corynebacterium glutamicum</i> aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the bmQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i> ,
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Giancotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambda diphtheriae," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(1):1819-1830 (1990)

Table 2 (continued)

	trpL; trpE	Putative leader peptide; anthranilate synthase component I	
X55994		Threonine synthase	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC		Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambda</i> corynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	Psl protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding Psl, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of Psl is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

	leuA	Isopropylmalate synthase	
X70959			Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pia-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,' <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360	Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361	Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362	Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363	Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Vrjlic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xyIB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

	glnA	Glutamine synthetase I	
Y13221			Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site <i>Corynebacterium</i> 304L	
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Moreau, S. et al. "Analysis of the integration functions of ϕ 304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21502	dapA; dapB		Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z29563	thrC	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z46753	16S rDNA	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z49822	sigA	Gene for 16S ribosomal RNA	
Z49823	galE; dtxR	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49824	orf1; sigB	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z66534		?, SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							
Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NGTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx000013	996	GB_GSS4:AQ713475	581	AQ713475	HS_5402_B2_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=978 Col=24 Row=B, genomic survey sequence.	Homo sapiens	37,148	13-Jul-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
rx000014	903	GB_BA1:MTCY3A2	25830	Z83867	Mycobacterium tuberculosis H37Rv complete genome; segment 136/162.	Mycobacterium tuberculosis	58,140	17-Jun-98
		GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	57,589	8-Aug-97
		GB_BA1:SAPURCLUS	9120	X92429	S.alboniger napH, pur7, pur10, pur6, pur4, pur5 and pur3 genes.	Sireptomyces anulatus	55,667	28-Feb-96
rx000030	513	GB_EST21:C89713	767	C89713	C89713 Dictyostelium discoideum SS (H.Urushiara) Dictyostelium discoideum cDNA clone SSG229, mRNA sequence.	Dictyostelium discoideum	45,283	20-Apr-98
		GB_EST28:A1497294	484	A1497294	fb63g03.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:AFP4_MYOC P80961 ANTIFREEZE PROTEIN LS-12. ., mRNA sequence.	Danio rerio	42,991	11-MAR-1999
		GB_EST21:C92167	637	C92167	C92167 Dictyostelium discoideum SS (H.Urushiara) Dictyostelium discoideum cDNA clone SSD179, mRNA sequence.	Dictyostelium discoideum	44,444	12-Jul-99
rx000032	1632	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	39,689	12-MAY-1998
		GB_BA2:AF018073	9810	AF018073	Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoF), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtlK), and periplasmic mannitol-binding protein (smoM) genes, complete cds.	Rhodobacter sphaeroides	48,045	22-OCT-1997
		GB_BA2:AF045245	5930	AF045245	Klebsiella pneumoniae D-arabinol transporter (dalT), D-arabinol kinase (dalK), D-arabinol dehydrogenase (dalD), and repressor (dalR) genes, complete cds.	Klebsiella pneumoniae	38,514	16-Jul-98
rx000041	1342	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	99,031	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	99,031	07-OCT-1996
		GB_IN1:LMFL5883	31934	AL117384	Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence.	Leishmania major	43,663	21-OCT-1999
rx000042	882	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	94,767	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	94,767	07-OCT-1996

Table 4 (continued)

rx000043	1287	GB_IN1:CEU33051 GB_PAT:126124 EM_PAT:E11760	4899 6911 6911	U33051 126124 E11760	Caenorhabditis elegans sur-2 mRNA, complete cds. Sequence 4 from patent US 5556776. Base sequence of sucrase gene.	Caenorhabditis elegans Unknown. Corynebacterium glutamicum	40,276 97,591 97,591	23-Jan-96 07-OCT-1996 08-OCT-1997 (Rel. 52, Created)
rx000098	1743	GB_PR3:AC005174 GB_BA1:MSU88433	39769 1928	AC005174 U88433	Homo sapiens clone UWGC:g1564a012 from 7p14-15, complete sequence. Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds.	Homo sapiens Mycobacterium smegmatis	35,879 62,658	24-Jun-98 19-Apr-97
rx000148	2334	GB_BA1:SC5A7 GB_BA1:MTCY10D7	40337 39800	AL031107 Z79700	Streptomyces coelicolor cosmid 5A7. Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Streptomyces coelicolor Mycobacterium tuberculosis	37,638 36,784	27-Jul-98 17-Jun-98
rx000148	2334	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	67,457	17-Jun-98
rx000149	1971	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	Mycobacterium tuberculosis	40,883	03-DEC-1996
rx000149	1971	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	Mycobacterium tuberculosis	67,457	10-DEC-1996
rx000149	1971	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	Mycobacterium tuberculosis	35,883	03-DEC-1996
rx000149	1971	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	Mycobacterium tuberculosis	51,001	10-DEC-1996
rx000195	684	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	51,001	17-Jun-98
rx000195	684	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	35,735	19-Jun-98
rx000196	738	GB_BA1:MSGB1529CS GB_BA1:MTCY274	36985 39991	L78824 Z74024	Mycobacterium leprae cosmid B1529 DNA sequence. Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium leprae Mycobacterium tuberculosis	57,014 41,892	15-Jun-96 19-Jun-98
rx000196	738	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	41,841	19-Jun-98
rx000202	1065	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	36,599	19-Jun-98
rx000202	1065	GB_RO:RATCIBRQ GB_EST11:AA253618	10752 313	M55532 AA253618	Rat carbohydrate binding receptor gene, complete cds. mw95c10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5' mRNA sequence.	Rattus norvegicus Mus musculus	36,212 38,816	27-Apr-93 13-MAR-1997
rx000202	1065	GB_EST26:AI390284	490	AI390284	mw96a03.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678508 5' similar to TR:O09171 O09171 BETTAINE-HOMOCYSTEINE METHYLTRANSFERASE., mRNA sequence.	Mus musculus	42,239	2-Feb-99
rx000206	1161	GB_EST26:AI390280	467	AI390280	mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5' mRNA sequence.	Mus musculus	37,307	2-Feb-99
rx000206	1161	GB_BA1:MLCB637 GB_BA1:MTV012	44882 70287	Z99263 AL021287	Mycobacterium leprae cosmid B637. Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium leprae Mycobacterium tuberculosis	58,312 36,632	17-Sep-97 23-Jun-99

Table 4 (continued)

GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10.	Streptomyces coelicolor A3(2)	38,616	5-Aug-99
GB_BA1:BUJ32230	1769	U32230	Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) nd large subunit (etfL) genes, complete cds.	Bradyrhizobium japonicum	48,038	25-MAY-1996
GB_BA1:PDEETFAB	2440	L14864	Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, complete cds's.	Paracoccus denitrificans	48,351	27-OCT-1993
GB_HTG3:AC009689	177954	AC009689	Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,756	28-Aug-99
GB_RO:AF060178	2057	AF060178	Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds.	Mus musculus	39,506	18-Jun-98
GB_GSS11:AQ325043	734	AQ325043	mgxb002J01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb002J01r, genomic survey sequence.	Magnaporthe grisea	38,333	8-Jan-99
GB_EST31:AI676413	551	AI676413	etmEST0167 Eimeria tenella cDNA clone etmc074 5', mRNA sequence.	Eimeria tenella	35,542	19-MAY-1999
GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	65,759	17-Jun-98
GB_BA2:AF061753	3721	AF061753	Nitrosomonas europaea CTP synthase (pyrG) gene, partial cds; and enolase (eno) gene, complete cds.	Nitrosomonas europaea	58,941	31-Aug-98
GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (nh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	61,239	4-Nov-98
GB_BA2:AF012550	2690	AF012550	Acinetobacter sp. BD413 ComP (comp) gene, complete cds.	Acinetobacter sp. BD413	53,726	27-Sep-99
GB_PAT:E03856	1506	E03856	gDNA encoding alcohol dehydrogenase.	Bacillus stearothermophilus	51,668	29-Sep-97
GB_BA1:BACADHT	1688	D90421	B. stearothermophilus adhT gene for alcohol dehydrogenase.	Bacillus	51,602	7-Feb-99
GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	42,875	17-Jun-98
GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	40,380	18-Jun-98
GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	41,789	18-Jun-98
GB_BA2:AF050114	1038	AF050114	Pseudomonas sp. W7 alginate lyase gene, complete cds.	Pseudomonas sp. W7	49,898	03-MAR-1999
GB_GSS3:B16984	469	B16984	344A14.TVC C1T978SKA1 Homo sapiens genomic clone A-344A14, genomic survey sequence.	Homo sapiens	39,355	4-Jun-98
GB_IN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (rpl34) gene, complete cds.	Aedes albopictus	36,509	3-Jun-99
GB_EST1:T28483	313	T28483	EST46182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monooxygenase 1 (HT:1956), mRNA sequence.	Homo sapiens	42,997	6-Sep-95

Table 4 (continued)

GB_PR1:HUMFMO1	2134	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.	Homo sapiens	37,915	8-Nov-94
GB_EST32:AI734238	512	AI734238	zb73c05.y5 Soares_fetal_lung_NHHL19W Homo sapiens cDNA clone IMAGE:309224 5' similar to gb:M64082 DIMETHYLANILINE MONOOXYGENASE (HUMAN);. mRNA sequence.	Homo sapiens	41,502	14-Jun-99
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 92 unordered pieces.	Drosophila melanogaster	33,890	02-DEC-1999
GB_EST15:AA531468	414	AA531468	np63d12.s1 NCL_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997175, mRNA sequence.	Homo sapiens	40,821	20-Aug-97
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 92 unordered pieces.	Drosophila melanogaster	30,963	02-DEC-1999
GB_VI:VMVY16780	186986	Y16780	variola minor virus complete genome.	variola minor virus	35,883	2-Sep-99
GB_VI:VARCG	186103	L22579	Variola major virus (strain Bangladesh-1975) complete genome.	Variola major virus	34,664	12-Jan-95
GB_VI:VWCGAA	185578	X69198	Variola virus DNA complete genome.	Variola virus	36,000	13-DEC-1996
GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	36,340	09-OCT-1998
GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	34,664	11-DEC-1992
GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	39,308	11-DEC-1992
GB_BA1:STYPUTPE	1887	L01138	Salmonella (S2980) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
GB_BA1:STYPUTPF	1887	L01139	Salmonella (S2983) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
GB_BA1:STYPUTPI	1889	L01142	Salmonella (S3015) proline permease (putP) gene, 5' end.	Salmonella sp.	42,906	09-MAY-1996
GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	38,142	16-MAY-1998
GB_PR4:AC004916	129014	AC004916	Homo sapiens clone DJ0891L14, complete sequence.	Homo sapiens	38,549	17-Jul-99
GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	35,865	16-MAY-1998
GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,940	24-Jun-99
GB_GSS12:AQ412290	238	AQ412290	RPCI-11-195H2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-195H2, genomic survey sequence.	Homo sapiens	36,555	23-MAR-1999
GB_PL2:AF112871	2394	AF112871	Astasia longa small subunit ribosomal RNA gene, complete sequence.	Astasia longa	36,465	28-Jun-99
GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99

Table 4 (continued)

	GB_PR2:HS134O19	86897	AL034555	Human DNA sequence from clone 134O19 on chromosome 1p36.11-36.33, complete sequence.	Homo sapiens	40,604	23-Nov-99
rx00381 729	GB_GSS4:AQ730532	416	AQ730532	HS_2149_A1_C06_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence.	Homo sapiens	35,766	15-Jul-99
	GB_EST23:A120939	561	A120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE); mRNA sequence.	Mus musculus	41,113	2-Sep-98
	GB_EST23:A120939	561	A120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE); mRNA sequence.	Mus musculus	41,113	2-Sep-98
rx00385 362	GB_EST32:A1726450	565	A1726450	BNLGH15857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence.	Gossypium hirsutum	41,152	11-Jun-99
	GB_GSS4:AQ740856	768	AQ740856	HS_2274_A2_A07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence.	Homo sapiens	41,360	16-Jul-99
	GB_PR1:HSPAIP	1587	X91809	H.sapiens mRNA for GAIP protein.	Homo sapiens	36,792	29-MAR-1996
rx00388 1134	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	51,852	17-Jun-98
	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	51,852	03-DEC-1996
	GB_HTG1:AP000471	72466	AP000471	Homo sapiens chromosome 21 clone B2308H15 map 21q22.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,875	13-Sep-99
rx00427 909	GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	60,022	10-DEC-1996
	GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	60,022	17-Jun-98
	GB_HTG1:CEY48C3	270193	Z92855	Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	28,013	29-MAY-1999
rx00483 1587	GB_PR2:HSFAF001550	173882	AF001550	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.	Homo sapiens	38,226	22-Aug-97
	GB_BA1:LLCPJW565	12828	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, abiM, abiR genes and orfX.	Lactococcus lactis subsp. cremoris	37,492	01-MAR-1999
	GB_HTG2:AC006754	206217	AC006754	Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS ***; 5 unordered pieces.	Caenorhabditis elegans	36,648	23-Feb-99
rx00511 615	GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	39,831	23-Nov-99
	GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	36,409	23-Nov-99
rx00512 718	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	56,232	17-Jun-98

Table 4 (continued)

	GB_BA1:MSGLTA	1776	X60513	M. smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	56,143	20-Sep-91
rxa00517 1164	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	48,563	14-Jul-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_EST29:AI602158	481	AI602158	UI-R-ABO-vy-a-01-O-UI.s2 UI-R-ABO Rattus norvegicus cDNA clone UI-R-ABO- vy-a-01-O-UI 3', mRNA sequence.	Rattus norvegicus	40,833	21-Apr-99
rxa00518 320	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	49,688	14-Jul-99
	GB_BA2:STU51879	8371	U51879	Salmonella typhimurium propionate catabolism operon: RpoN activator protein homolog (prpR), carboxyphosphoenolpyruvate phosphonmutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds.	Salmonella typhimurium	50,313	5-Aug-99
rxa00606 2378	GB_BA2:AE000140	12498	AE000140	Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome.	Escherichia coli	49,688	12-Nov-98
	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,333	7-Jun-99
	GB_EST13:AA363046	329	AA363046	EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	34,347	21-Apr-97
	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,899	7-Jun-99
rxa00635 1860	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloclavata DNA for ORF 1.	Pseudomonas amyloclavata	53,912	14-Jul-95
	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloclavata DNA for ORF 1.	Pseudomonas amyloclavata	54,422	14-Jul-95
rxa00679 1389	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	38,244	13-Nov-99
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	36,091	12-MAR-1997
rxa00680 441	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	37,135	13-Nov-99
	GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	36,165	30-Sep-98
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	38,732	12-MAR-1997
	GB_PL1:AB026648	43481	AB026648	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence.	Arabidopsis thaliana	38,732	07-MAY-1999
rxa00682 2022	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	37,143	28-Sep-99

Table 4 (continued)

rx00683	1215	GB_BA2:AE000896	10707	AE000896	Methanobacterium thermoautotrophicum (section 102 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	38,429	15-Nov-97
		GB_IN1:DMBRTA4	212734	AL109630	Drosophila melanogaster clone BACR7A4.	Drosophila melanogaster	36,454	30-Jul-99
		GB_EST35:AV163010	273	AV163010	AV163010 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA clone 3110006J22, mRNA sequence.	Mus musculus	41,758	8-Jul-99
rx00686	927	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_EST12:AA284399	431	AA284399	zs57b04.r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701551 5', mRNA sequence.	Homo sapiens	39,205	14-Aug-97
rx00700	927	GB_EST34:A1785570	454	A1785570	uj44d03.x1 Sugano mouse liver mla Mus musculus cDNA clone IMAGE:1922789 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	Mus musculus	41,943	2-Jul-99
		GB_EST25:A1256147	684	A1256147	uj95e12.x1 Sugano mouse liver mla Mus musculus cDNA clone IMAGE:1890190 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	Mus musculus	40,791	12-Nov-98
rx00703	2409	GB_BA1:CARCG12	2079	X14979	C. aurantiacus reaction center genes 1 and 2.	Chloroflexus aurantiacus	37,721	23-Apr-91
		GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	56,646	2-Aug-99
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,369	19-Jun-98
		GB_BA2:REU60056	2520	U60056	Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds.	Ralstonia eutropha	51,087	16-OCT-1996
rx00705	1038	GB_GSS15:AQ604477	505	AQ604477	HS_2116_B1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence.	Homo sapiens	39,617	10-Jun-99
		GB_EST11:AA224340	443	AA224340	zr14e07.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648804 3', mRNA sequence.	Homo sapiens	35,129	11-MAR-1998
		GB_EST5:N30648	291	N30648	yw77b02.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258219 3', mRNA sequence.	Homo sapiens	43,986	5-Jan-96
rx00782	1005	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Mycobacterium tuberculosis	63,327	17-Jun-98
		GB_BA1:MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	62,300	27-Aug-99
		GB_BA2:AF128399	2842	AF128399	Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (sucC) and succinyl-CoA synthetase alpha subunit (sucD) genes, complete cds.	Pseudomonas aeruginosa	53,698	25-MAR-1999
rx00783	1395	GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***; 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
		GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***; 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
rx00794	1128	GB_PR3:AC005017	137176	AC005017	Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.	Homo sapiens	35,864	8-Aug-98
		GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	40,331	24-Jun-99

Table 4 (continued)

GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,170	27-Aug-99
GB_PR2:HS151B14	128942	Z82188	Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene, pseudogene similar to ribosomal protein L39, RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSs, GSSs and CpG islands, complete sequence.	Homo sapiens	37,455	16-Jun-99
GB_PL2:AF016327	616	AF016327	Hordeum vulgare Barpermi1 (perm1) mRNA, partial cds.	Hordeum vulgare	41,311	01-OCT-1997
GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	63,101	17-Jun-98
GB_BA1:AB019513	4417	AB019513	Streptomyces coelicolor genes for alcohol dehydrogenase and ABC transporter, complete cds.	Streptomyces coelicolor	41,312	13-Nov-98
GB_PL1:SCSFAARP	7008	X68020	S.cerevisiae SFA and ARP genes.	Saccharomyces cerevisiae	36,288	29-Nov-94
GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	39,980	17-Jun-98
GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	39,435	27-Aug-99
GB_BA2:AF169031	1141	AF169031	Xanthomonas oryzae pv. oryzae putative sugar nucleotide epimerase/dehydratase gene, partial cds.	Xanthomonas oryzae pv. oryzae	46,232	14-Sep-99
GB_IN1:CEF23H12	35564	Z74472	Caenorhabditis elegans cosmid F23H12, complete sequence.	Caenorhabditis elegans	34,502	08-OCT-1999
GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
GB_BA1:MTV049	40360	AL022021	Mycobacterium tuberculosis H37Rv complete genome; segment 81/162.	Mycobacterium tuberculosis	36,981	19-Jun-98
GB_PL2:CDU236897	1827	AJ236897	Candida dubliniensis ACT1 gene, exons 1-2.	Candida dubliniensis	38,716	1-Sep-99
GB_PL1:CAACT1A	3206	X16377	Candida albicans act1 gene for actin.	Candida albicans	36,610	10-Apr-93
GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	51,586	12-MAY-1998
GB_BA1:RMPHA	7888	X93358	Rhizobium meliloti pha(A,B,C,D,E,F,G) genes.	Sinorhizobium meliloti	48,367	12-MAR-1999
GB_EST16:C23528	317	C23528	C23528 Japanese flounder spleen Paralicthys olivaceus cDNA clone HB5(2), mRNA sequence.	Paralicthys olivaceus	41,640	28-Sep-99
GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_Q_1 map 18, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99

Table 4 (continued)

GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS ***. 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99
GB_EST18:AA709478	406	AA709478	v34a05.11 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1224272 5', mRNA sequence.	Mus musculus	42,065	24-DEC-1997
GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***. 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***. 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
GB_BA1:MTCY05A6	38631	Z96072	Mycobacterium tuberculosis H37Rv complete genome; segment 120/162.	Mycobacterium tuberculosis	36,218	17-Jun-98
rx000965						
GB_PAT:E13660	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase.	Corynebacterium glutamicum	98,349	24-Jun-98
GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	38,520	17-Jun-98
GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	64,355	27-Aug-99
GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,860	17-Jun-98
GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,120	17-Jun-98
GB_BA1:SC7A1	32039	AL034447	Streptomyces coelicolor cosmid 7A1.	Streptomyces coelicolor	55,287	15-DEC-1998
GB_BA1:MSGB173CS	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae	56,847	15-Jun-96
GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	56,676	17-Sep-97
GB_BA2:AF017444	3067	AF017444	Sinorhizobium meliloti NADP-dependent malic enzyme (tme) gene, complete cds.	Sinorhizobium meliloti	53,660	2-Nov-97
GB_BA1:BSUB0013	218470	Z99116	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730.	Bacillus subtilis	37,255	26-Nov-97
GB_VI:HSV2HG52	154746	Z86099	Herpes simplex virus type 2 (strain HG52), complete genome.	human herpesvirus 2	38,081	04-DEC-1998
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone BWXD20, *** SEQUENCING IN PROGRESS ***. 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone BWXD20, *** SEQUENCING IN PROGRESS ***. 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone BWXD20, *** SEQUENCING IN PROGRESS ***. 11 unordered pieces.	Homo sapiens	26,180	2-Sep-97
GB_PR3:HSDJ653C5	85237	AL049743	Human DNA sequence from clone 553C5 on chromosome 1p21.3-22.3 Contains CA repeat(D1S435), STSs and GSSs, complete sequence.	Homo sapiens	36,462	23-Nov-99
GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	41,808	1-Jul-95
GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	36,130	1-Jul-95
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18 TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	36,528	14-Jul-98

Table 4 (continued)

GB_GSS8:AQ042907	392	AQ042907	CIT-HSP-2318D17. TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence.	Homo sapiens	35,969	14-Jul-98
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18. TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	44,545	14-Jul-98
GB_BA1:CORPYK1	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	Corynebacterium glutamicum	100,000	07-DEC-1994
GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	63,771	17-Jun-98
GB_BA1:MIU65430	1439	U65430	Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds.	Mycobacterium intracellulare	67,061	23-DEC-1996
GB_BA2:AF045998	780	AF045998	Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds.	Corynebacterium glutamicum	99,615	19-Feb-98
GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	100,000	12-MAR-1998
GB_GSS1:FR0005503	619	Z89313	F. rubripes GSS sequence, clone 079B16aE8, genomic survey sequence.	Fugu rubripes	37,785	01-MAR-1997
GB_PR3:AC004063	177014	AC004063	Homo sapiens chromosome 4 clone B3218, complete sequence.	Homo sapiens	35,835	10-Jul-98
GB_PR3:HS1178121	62268	AL109852	Human DNA sequence from clone RP5-1178121 on chromosome X, complete sequence.	Homo sapiens	37,873	01-DEC-1999
GB_HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS *** , 5 unordered pieces.	Homo sapiens	37,240	13-Aug-99
GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
GB_IN1:DMC66A1	34127	AL031227	Drosophila melanogaster cosmid 66A1.	Drosophila melanogaster	38,416	05-OCT-1998
GB_BA1:CGASO19	1452	X76875	C. glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	99,931	27-OCT-1994
EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	99,242	07-OCT-1997 (Rel. 52, Created)
GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,153	09-MAR-1995
EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	100,000	07-OCT-1997 (Rel. 52, Created)
GB_BA1:CGASO19	1452	X76875	C. glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	100,000	27-OCT-1994
GB_Vi:HEPCRE4B	414	X60570	Hepatitis C genomic RNA for putative envelope protein (RE4B isolate).	Hepatitis C virus	36,769	5-Apr-92

rxa01200

Table 4 (continued)

rx01201 1764	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	66,269	01-MAY-1995
	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	65,437	17-Jun-98
	GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,302	09-MAR-1995
rx01202 1098	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	57,087	01-MAY-1995
	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	38,298	01-MAY-1995
	GB_BA1:MCSQSSHC	5538	Y09978	M.capsulatus orfz, orfz, sqs and shc genes.	Methylococcus capsulatus	37,626	26-MAY-1998
rx01204 933	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain: Columbia.	Chloroplast Arabidopsis thaliana	38,395	15-Sep-99
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS ***; 39 unordered pieces.	Homo sapiens	35,459	04-DEC-1999
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS ***; 39 unordered pieces.	Homo sapiens	36,117	04-DEC-1999
rx01216 1124	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	39,064	17-Jun-98
	GB_BA2:AF017435	4301	AF017435	Methylobacterium extorquens methanol oxidation genes, glmU-like gene, partial cds, and orfL2, orfL1, orfR genes, complete cds.	Methylobacterium extorquens	42,671	10-MAR-1998
	GB_BA1:CORFLBDBA	4424	M59228	C.crescentus flagellar gene promoter region.	Caulobacter crescentus	41,054	26-Apr-93
rx01225 1563	GB_BA2:AF058302	25306	AF058302	Streptomyces roseofulvus frenolicin biosynthetic gene cluster, complete sequence.	Streptomyces roseofulvus	36,205	2-Jun-98
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 O4.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 O4.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
rx01227 444	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	64,908	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	62,838	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	61,712	10-DEC-1996
rx01242 900	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	35,373	09-OCT-1998
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS ***; 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS ***; 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99

Table 4 (continued)

rx01243 1083	GB_GSS10:AQ255057	583	AQ255057	mgxb0008N01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008N01r, genomic survey sequence.	Magnaporthe grisea	38,722	23-OCT-1998
rx01259 981	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,448	23-Nov-98
	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,694	23-Nov-98
	GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPC198-11N6, *** SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
rx01262 1284	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPC198-11N6, *** SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
	GB_BA2:AF172324	14263	AF172324	Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds; and chain length determinant Wzz (wzz) gene, partial cds.	Escherichia coli	59,719	29-OCT-1999
	GB_BA2:ECU78086	4759	U78086	Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and O-chain length regulator (wzz) genes, complete cds.	Escherichia coli	59,735	5-Nov-97
	GB_BA1:D90841	20226	D90841	E.coli genomic DNA, Kohara clone #351(45.1-45.5 min.).	Escherichia coli	37,904	21-MAR-1997
rx01311 870	GB_PR3:AC004103	144368	AC004103	Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	37,340	18-Apr-98
	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
	GB_BA2:AE000487	13889	AE000487	Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome.	Escherichia coli	39,494	12-Nov-98
rx01312 2142	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	46,252	23-Jun-99
	GB_BA1:U00022	36411	U00022	Mycobacterium leprae cosmid L308.	Mycobacterium leprae	46,368	01-MAR-1994
	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
rx01325 795	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	39,618	2-Nov-99
	GB_HTG6:AC007186	225851	AC007186	Drosophila melanogaster chromosome 2 clone BACR03D06 (D569) RPC1-98 03.D.6 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 91 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
	GB_HTG6:AC007147	202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPC1-98 19.N.18 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
	GB_HTG6:AC007147	202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPC1-98 19.N.18 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999

Table 4 (continued)

GB_HTG3:AC010207	207890	AC010207	Homo sapiens clone RPC111-375120, *** SEQUENCING IN PROGRESS ***; 25 Homo sapiens unordered pieces.	34,821	16-Sep-99
GB_BA2:AF109682	990	AF109682	Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds.	58,487	19-OCT-1999
GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	37,963	25-Feb-99
GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	37,963	25-Feb-99
GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	38,011	17-Jun-98
GB_BA1:XANXANAB	3410	M83231	Xanthomonas campestris phosphoglucomutase and phosphomannomutase (xanA) and phosphomannose isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds.	47,726	26-Apr-93
GB_GSS10:AQ194038	697	AQ194038	RPC111-47D24.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-47D24, genomic survey sequence.	36,599	20-Apr-99
GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	36,940	17-Jun-98
GB_GSS3:B10037	974	B10037	T27A19-T7 TAMU Arabidopsis thaliana genomic clone T27A19, genomic survey sequence.	35,284	14-MAY-1997
GB_GSS3:B09549	1097	B09549	T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence.	38,324	14-MAY-1997
GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	39,778	10-Feb-99
GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252018, WORKING DRAFT SEQUENCE, 121 unordered pieces.	32,658	16-Nov-99
GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252018, WORKING DRAFT SEQUENCE, 121 unordered pieces.	38,395	16-Nov-99
GB_BA2:AF072709	8366	AF072709	Streptomyces lividans amplifiable element AUD4: putative transcriptional regulator, putative ferredoxin, putative cytochrome oxidoreductase, and putative oxidoreductase genes, complete unknown genes.	55,221	8-Jul-98
GB_BA1:CGLYSEG	2374	X96471	C. glutamicum lysE and lysG genes.	100,000	24-Feb-97
GB_PR4:AC005906	185952	AC005906	Homo sapiens 12p13.3 BAC RPC111-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	36,756	30-Jan-99
GB_BA1:CGPTAACKA	3657	X89084	C. glutamicum pta gene and ackA gene.	100,000	23-MAR-1999
GB_BA1:D90861	14839	D90861	E. coli genomic DNA, Kohara clone #405(52.0-52.3 min.).	53,041	29-MAY-1997
GB_PAT:E02087	1200	E02087	DNA encoding acetate kinase protein from Escherichia coli.	54,461	29-Sep-97
GB_GSS1:HPJ06027	280	U60627	Helicobacter pylori feoB-like DNA sequence, genomic survey sequence.	39,286	9-Apr-97
GB_EST31:A1701691	349	A1701691	we81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347494 3' similar to gb.L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);, mRNA sequence.	39,412	3-Jun-99

Table 4 (continued)

GB_EST15:AA480256	389	AA480256	ne31f04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898975 3' similar to gb:L19686_ma1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);, mRNA sequence.	Homo sapiens	39,574	14-Aug-97
rxa01478 1959						
GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	54,141	15-Aug-99
GB_BA1:SCE36	12581	AL049763	Streptomyces coelicolor cosmid E36.	Streptomyces coelicolor	38,126	05-MAY-1999
GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,852	9-Apr-97
GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	62,149	20-Aug-98
GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	38,303	01-MAR-1994
GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome, segment 146/162.	Mycobacterium tuberculosis	38,179	18-Jun-98
rxa01534						
GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	66,208	27-Aug-99
GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome, segment 48/162.	Mycobacterium tuberculosis	38,553	24-Jun-99
GB_BA1:PAU72494	4368	U72494	Pseudomonas aeruginosa fumarase (fumC) and Mn superoxide dismutase (sodA) genes, complete cds.	Pseudomonas aeruginosa	52,690	23-OCT-1996
GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	Synechocystis sp.	56,487	7-Feb-99
GB_IN2:AF073177	9534	AF073177	Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds.	Drosophila melanogaster	55,100	1-Jul-99
GB_IN2:AF073179	3159	AF073179	Drosophila melanogaster glycogen phosphorylase (GlyP) mRNA, complete cds.	Drosophila melanogaster	56,708	27-Apr-99
rxa01562						
GB_BA1:D78182	7836	D78182	Streptococcus mutans DNA for dTDP-rhamnose synthesis pathway, complete cds.	Streptococcus mutans	44,050	5-Feb-99
GB_BA2:AF079139	4342	AF079139	Streptomyces venezuelae pikCD operon, complete sequence.	Streptomyces venezuelae	38,587	28-OCT-1998
GB_BA2:AF087022	1470	AF087022	Streptomyces venezuelae cytochrome P450 monooxygenase (picK) gene, complete cds.	Streptomyces venezuelae	38,621	15-OCT-1998
GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome, segment 16/162.	Mycobacterium tuberculosis	59,035	17-Jun-98
GB_BA2:AF097519	4594	AF097519	Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (mlb), glucose-1-phosphate thymidyl transferase (rmlA), dTDP-4-keto-L-rhamnose reductase (rmlD), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (rmlC), and rhamnosyl transferase (wbbL) genes, complete cds.	Klebsiella pneumoniae	59,714	4-Nov-98

Table 4 (continued)

GB_BA2:NGOCSPS	8905	L09189	Neisseria meningitidis dTDP-D-glucose 4,6-dehydratase (rfbB), glucose-1-phosphate thymidyl transferase (rfbA) and rfbC genes, complete cds and UPD-glucose-4-epimerase (galE) pseudogene.	Neisseria meningitidis	58,384	30-Jul-96
GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,500	7-Aug-98
GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	35,655	7-Aug-98
GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,843	7-Aug-98
GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	38,119	7-Aug-98
GB_Vi:CFU72240	4783	U72240	Choristoneura fumiferana nuclear polyhedrosis virus ETM protein homolog, 79 kDa protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds.	Choristoneura fumiferana nucleopolyhedrovirus	37,115	29-Jan-99
GB_GSS10:AQ213248	408	AQ213248	HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence.	Homo sapiens	34,559	18-Sep-98
GB_GSS8:AQ070145	285	AQ070145	HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence.	Homo sapiens	40,351	5-Aug-98
GB_PR4:AF152510	2490	AF152510	Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds.	Homo sapiens	34,298	14-Jul-99
GB_PR4:AF152323	4605	AF152323	Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds.	Homo sapiens	34,298	22-Jul-99
GB_PR4:AF152509	2712	AF152509	Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence.	Homo sapiens	34,298	14-Jul-99
GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N:2 map 36E-36E strain y; cn bw sp. *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N:2 map 36E-36E strain y; cn bw sp. *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
GB_GSS8:B99182	415	B99182	CIT-HSP-2280113. TR CIT-HSP Homo sapiens genomic clone 2280113, genomic survey sequence.	Homo sapiens	36,111	26-Jun-98
GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200. Bacillus subtilis	Bacillus subtilis	36,591	26-Nov-97
GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200. Bacillus subtilis	Bacillus subtilis	34,941	26-Nov-97
GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp. *** SEQUENCING IN PROGRESS***, 17 unordered pieces.	Drosophila melanogaster	37,037	2-Aug-99

Table 4 (continued)

rx01695 1623	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	100,000	11-Aug-98
	GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	Mycobacterium tuberculosis	38,626	17-Jun-98
rx01702 1155	GB_IN1:DMU15974	2994	U15974	Drosophila melanogaster kinesin-like protein (klp68d) mRNA, complete cds.	Drosophila melanogaster	36,783	18-Jul-95
	GB_BA1:CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13).	Corynebacterium glutamicum	99,913	12-Sep-93
	GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	38,786	17-Jun-98
rx01743 901	GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	38,238	27-Aug-99
	GB_IN2:CELC27H5	35840	U14635	Caenorhabditis elegans cosmid C27H5.	Caenorhabditis elegans	35,334	13-Jul-95
	GB_EST24:AI167112	579	AI167112	xylem.est.878 Poplar xylem Lambda ZAPII library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence.	Populus balsamifera subsp. trichocarpa	39,222	03-DEC-1998
	GB_GSS9:AQ102635	347	AQ102635	HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence.	Homo sapiens	40,653	27-Aug-98
rx01744 1662	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	36,650	17-Jun-98
	GB_GSS1:AF009226	665	AF009226	Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence, genomic survey sequence.	Mycobacterium tuberculosis	53,438	31-Jul-97
rx01745 836	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	53,088	26-Nov-98
	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	52,081	17-Jun-98
	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,364	22-Aug-97
rx01758 1140	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	52,323	12-Nov-98
	GB_PR3:HS57G9	113872	Z95116	Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.	Homo sapiens	39,209	23-Nov-99
	GB_PL2:YSCH9666	39057	U10397	Saccharomyces cerevisiae chromosome VIII cosmid 9666.	Saccharomyces cerevisiae	40,021	5-Sep-97
	GB_PL2:YSCH9986	41664	U00027	Saccharomyces cerevisiae chromosome VIII cosmid 9986.	Saccharomyces cerevisiae	34,375	29-Aug-97
rx01814 1785	GB_BA1:ABCCLEB	2058	L24077	Acetobacter xylinum phosphoglucomutase (celB) gene, complete cds.	Acetobacter xylinus	62,173	21-Sep-94
	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	39,749	17-Jun-98
	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	40,034	17-Jun-98
rx01851 1809	GB_GSS9:AQ142579	529	AQ142579	HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence.	Homo sapiens	38,068	24-Sep-98
	GB_IN2:AC005889	108924	AC005889	Drosophila melanogaster, chromosome 2L, region 30A3-30A6, P1 clones DS06958 and DS03097, complete sequence.	Drosophila melanogaster	36,557	30-OCT-1998
	GB_GSS1:AG008814	637	AG008814	Homo sapiens genomic DNA, 21q region, clone: B137B7BB68, genomic survey sequence.	Homo sapiens	35,316	7-Feb-99

Table 4 (continued)

rx01859 1050	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,364	03-OCT-1999
	GB_HTG5:AC008031	158889	AC008031	Trypanosoma brucei chromosome II clone RPC193-25N14, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Trypanosoma brucei	35,334	15-Nov-99
	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,529	03-OCT-1999
rx01865 438	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	59,862	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	61,949	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	59,908	10-DEC-1996
rx01882 1113	GB_PR1:HUMADRA2C	1491	J03853	Human kidney alpha-2-adrenergic receptor mRNA, complete cds.	Homo sapiens	36,899	27-Apr-93
	GB_PR4:HSU72648	4850	U72648	Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.	Homo sapiens	36,899	23-Nov-98
	GB_GSS3:B42200	387	B42200	HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence.	Homo sapiens	34,805	18-OCT-1997
rx01884 1913	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	37,892	17-Jun-98
	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	40,413	29-MAR-1999
rx01886 897	GB_BA1:D90908	122349	D90908	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234.	Synechocystis sp.	47,792	7-Feb-99
	GB_GSS9:AQ116291	572	AQ116291	RPC111-49P6.TK.1 RPC1-11 Homo sapiens genomic clone RPC1-11-49P6, genomic survey sequence.	Homo sapiens	43,231	20-Apr-99
	GB_BA2:AE001721	17632	AE001721	Thermotoga maritima section 33 of 136 of the complete genome.	Thermotoga maritima	39,306	2-Jun-99
	GB_EST16:AA567090	596	AA567090	GM01044.5prime GM Drosophila melanogaster ovary Bluescript Drosophila melanogaster cDNA clone GM01044.5prime, mRNA sequence.	Drosophila melanogaster	42,807	28-Nov-98
rx01887 1134	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	36,417	03-DEC-1999
	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	37,667	03-DEC-1999
	GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwoffii wcz, wzb, wza, weeA, weeB, weeC, wzc, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwoffii	39,640	01-OCT-1999
rx01888 658	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPC1-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99

Table 4 (continued)

GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***; 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99
GB_EST36:AI881527	598	AI881527	606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, Zea mays mRNA sequence.		43,617	21-Jul-99
GB_VI:HIV232971	621	AJ232971	Human immunodeficiency virus type 1 subtype C nef gene, patient MP83.	Human immunodeficiency virus type 1	40,040	05-MAR-1999
GB_PL1:AFCHSE	6158	Y09542	A.fumigatus chsE gene.	Aspergillus fumigatus	37,844	1-Apr-97
GB_PR3:AF064858	193387	AF064858	Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence.	Homo sapiens	37,136	2-Jun-98
GB_BA1:CGL238250	1593	AJ238250	Corynebacterium glutamicum ndh gene.	Corynebacterium glutamicum	100,000	24-Apr-99
GB_BA2:AF038423	1376	AF038423	Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds.	Mycobacterium smegmatis	65,254	05-MAY-1998
GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	40,058	17-Jun-98
GB_BA1:MSGB38COS	37114	L01095	M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds.	Mycobacterium leprae	59,551	6-Sep-94
GB_BA1:SCFE63	37200	AL035640	Streptomyces coelicolor cosmid E63.	Streptomyces coelicolor	39,468	17-MAR-1999
GB_PR3:AF093117	147216	AF093117	Homo sapiens chromosome 7q10 BAC E3, complete sequence.	Homo sapiens	39,291	02-OCT-1998
GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	38,384	11-MAY-1999
GB_BA1:ASXYLA	1905	X59466	Arthrobacter Sp. N.R.L. B3728 xylA gene for D-xylose(D-glucose) isomerase.	Arthrobacter sp.	56,283	04-MAY-1992
GB_HTG3:AC009500	176060	AC009500	Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS ***; 6 unordered pieces.	Homo sapiens	37,593	24-Aug-99
GB_BA2:AE000739	13335	AE000739	Aquifex aeolicus section 71 of 109 of the complete genome.	Aquifex aeolicus	36,309	25-MAR-1998
GB_EST28:AI519629	612	AI519629	LD39282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD39282 5prime, mRNA sequence.	Drosophila melanogaster	41,941	16-MAR-1999
GB_EST21:AA949396	767	AA949396	LD28277.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28277 5prime, mRNA sequence.	Drosophila melanogaster	39,855	25-Nov-98
GB_BA1:BSPGIA	1822	X16639	Bacillus stearothermophilus pgIA gene for phosphoglucosomerase isoenzyme A (EC 5.3.1.9).	Bacillus stearothermophilus	66,292	20-Apr-95
GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	Bacillus subtilis	37,255	26-Nov-97
GB_BA2:AF132127	8452	AF132127	Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene.	Streptococcus mutans	63,607	28-Sep-99
GB_BA1:SXSCRBA	3161	X67744	S.xyloosus scrB and scrR genes.	Staphylococcus xyloosus	67,778	28-Nov-96
GB_BA1:BSUB0020	212150	Z99123	Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.	Bacillus subtilis	35,574	26-Nov-97
GB_BA1:BSGENR	97015	X73124	B.subtilis genomic region (325 to 333).	Bacillus subtilis	51,826	2-Nov-93
GB_BA1:MTIC237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome; segment 46/162.	Mycobacterium tuberculosis	54,476	17-Jun-98

Table 4 (continued)

	GB_PL2:SCE9537	66030	U18778	Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898.	Saccharomyces cerevisiae	36,100	1-Aug-97
	GB_GSS13:AQ501177	767	AQ501177	V26G9 mTr-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', Saccharomyces cerevisiae genomic survey sequence.	Saccharomyces cerevisiae	32,039	29-Apr-99
rxa02054	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,896	27-Aug-99
	GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	59,964	17-Jun-98
rxa02056	GB_BA1:MTU43540	3453	U43540	Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds.	Mycobacterium tuberculosis	59,659	14-Aug-97
	GB_PAT:E14601	4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	98,928	28-Jul-99
	GB_BA1:D84102	4394	D84102	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds.	Corynebacterium glutamicum	98,928	6-Feb-99
	GB_BA1:MTV006	22440	AL021006	Mycobacterium tuberculosis H37Rv complete genome; segment 54/162.	Mycobacterium tuberculosis	39,265	18-Jun-98
rxa02061	GB_HTG7:AC005883	211682	AC005883	Homo sapiens chromosome 17 clone RP11-958E11 map 17, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	37,453	08-DEC-1999
	GB_PL2:ATAC003033	84254	AC003033	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	19-DEC-1997
rxa02063	GB_PL2:ATAC002334	75050	AC002334	Arabidopsis thaliana chromosome II BAC F25118 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	04-MAR-1998
	GB_BA1:SCGLGC	1518	X89733	S.coelicolor DNA for glgC gene.	Streptomyces coelicolor	56,972	12-Jul-99
	GB_GSS4:AQ687350	786	AQ687350	nbxb0074H11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0074H11r, genomic survey sequence.	Oryza sativa	40,696	1-Jul-99
	GB_EST36:AW028530	444	AW028530	ww27f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:25307953 similar to WP:T03G11.6 CE04874; mRNA sequence.	Homo sapiens	36,795	27-OCT-1999
rxa02100	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	40,156	10-DEC-1996
	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	55,218	17-Jun-98
rxa02122	GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterl.	Streptomyces coelicolor	38,475	29-MAR-1999
	GB_BA1:D90858	13548	D90858	E.coli genomic DNA, Kohara clone #401(51.3-51.6 min.).	Escherichia coli	38,586	29-MAY-1997
	GB_EST37:AI948595	469	AI948595	wq07d12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:24705833; mRNA sequence.	Homo sapiens	37,259	6-Sep-99
rxa02140	GB_HTG3:AC010387	220665	AC010387	Homo sapiens chromosome 5 clone CITB-H1_2074D8, *** SEQUENCING IN PROGRESS ***; 77 unordered pieces.	Homo sapiens	38,868	15-Sep-99
	GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
	GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
	GB_RO:AF093099	2482	AF093099	Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds.	Mus musculus	36,683	01-OCT-1999
rxa02142	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,292	17-Jun-98

Table 4 (continued)

GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,058	24-MAR-1999
GB_BA1:AB016787	5550	AB016787	Pseudomonas putida genes for cytochrome o ubiquinol oxidase A-E and 2 ORFs, complete cds.	Pseudomonas putida	47,403	5-Aug-99
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,317	17-Jun-98
GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	55,530	17-Jun-98
GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
GB_EST28:AI492095	485	AI492095	tg07a01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108040 3', mRNA sequence.	Homo sapiens	39,798	30-MAR-1999
GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
GB_PR3:HSBK277P6	61698	AL117347	Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence.	Homo sapiens	36,872	23-Nov-99
GB_BA2:EMB065R075	360	AF116423	Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence.	Rhizobium etli	43,175	06-DEC-1999
GB_EST34:AI789323	574	AI789323	uk53g05.y1 Sugano mouse kidney mRna Mus musculus cDNA clone IMAGE:1972760 5' similar to WP:K11H12.8 CE12160 ; mRNA sequence.	Mus musculus	39,715	2-Jul-99
GB_BA1:CGGLTG	3013	X66112	C. glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	100,000	17-Feb-95
GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	64,331	17-Jun-98
GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid B57.	Mycobacterium leprae	62,491	10-Feb-99
GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	38,791	31-MAY-1995
GB_GSS8:AQ012162	763	AQ012162	127PB037070197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127PB037070197, genomic survey sequence.	Rhodobacter sphaeroides	40,044	4-Jun-98
GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	37,312	31-MAY-1995
GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,173	3-Apr-99
GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasins 1 (inv1), invasins 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	40,219	26-MAR-1998

Table 4 (continued)

rx02213 874	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	38,253	17-Jun-98
	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,096	3-Apr-99
	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	34,937	17-Jun-98
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	36,885	26-MAR-1998
rx02245 780	GB_BA2:RCU23145	5960	U23145	Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-/sedoheptulose-1,7-bisphosphate aldolase (cbbA) gene, partial cds, Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon: pentose-5-phosphate-3-epimerase (cbbE), phosphoglycerate phosphatase (cbbZ), and cbbY genes, complete cds.	Rhodobacter capsulatus	48,701	28-OCT-1997
rx02256 1125	GB_BA1:CGGAPPGK	3804	X59403	Escherichia coli minutes 9 to 11 genomic sequence.	Escherichia coli	39,119	11-Jan-97
	GB_BA1:SCC54	30753	AL035591	Homo sapiens chromosome 18 clone HRPK 178_F_10 map 18, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces.	Homo sapiens	33,118	26-Jun-99
	GB_BA1:MTCY493	40790	Z95844	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,289	05-OCT-1992
rx02257 1338	GB_BA1:CGGAPPGK	3804	X59403	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	36,951	11-Jun-99
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	64,196	19-Jun-98
	GB_BA2:MAU82749	2530	U82749	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	98,873	05-OCT-1992
rx02258 900	GB_BA1:CGGAPPGK	3804	X59403	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	61,273	19-Jun-98
	GB_BA1:CORPEPC	4885	M25819	Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds.	Mycobacterium avium	61,772	6-Jan-98
	GB_PAT:A09073	4885	A09073	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,667	05-OCT-1992
rx02259 2895	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
	GB_BA1:CGPPC	3292	X14234	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
				C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
				Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4.1.1.31).	Corynebacterium glutamicum	99,827	12-Sep-93

Table 4 (continued)

rx02288 969	GB_PR3:HSDJ94E24	243145	AL050317	Human DNA sequence from clone RP1-94E24 on chromosome 20q12, complete sequence.	Homo sapiens	36,039	03-DEC-1999
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS *** 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS *** 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
rx02292 798	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	39,747	01-DEC-1999
	GB_GSS5:AQ744695	827	AQ744695	HS_5505_A2_C06_SP6 RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=12 Row=E, genomic survey sequence.	Homo sapiens	39,185	16-Jul-99
	GB_EST14:AA381925	309	AA381925	EST95058 Activated T-cells 1 Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	35,922	21-Apr-97
rx02322 511	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	57,677	17-Jun-98
	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	37,143	17-Jun-98
rx02326 939	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
	GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	37,363	17-Jun-98
rx02327 1083	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	99,259	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	99,259	24-DEC-1997
	GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	41,317	17-Jun-98
rx02328 1719	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
rx02332 1266	GB_PL2:AF097728	3916	AF097728	Aspergillus terreus pyruvate carboxylase (Pyc) mRNA, complete cds.	Aspergillus terreus	52,248	29-OCT-1998
	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,460	20-Sep-91
	GB_BA2:ABU85944	1334	U85944	Antarctic bacterium DS2-3R citrate synthase (cisy) gene, complete cds.	Antarctic bacterium DS2-3R	57,154	23-Sep-97
rx02333 1038	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	38,164	12-Nov-98
	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,929	20-Sep-91
	GB_PR4:HUAC002299	171681	AC002299	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 ~complete genomic sequence, complete sequence.	Homo sapiens	33,070	23-Nov-99

Table 4 (continued)

rx02399 1467	GB_HTG2:AC007889	127840	AC007889	Drosophila melanogaster chromosome 3 clone BACR48E12 (D695) RPCI-98 48.E.12 map 87A-87B strain y; on bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces.	Drosophila melanogaster	34,897	2-Aug-99
	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
	GB_BA1:CORACEA	1905	L28760	Corynebacterium glutamicum isocitrate lyase (aceA) gene.	Corynebacterium glutamicum	100,000	10-Feb-95
rx02404 2340	GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	99,795	26-Sep-95
	GB_BA1:CGACEB	3024	X78491	C.glutamicum (ATCC 13032) aceB gene.	Corynebacterium glutamicum	99,914	13-Jan-95
	GB_BA1:CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds.	Corynebacterium glutamicum	99,786	8-Jun-95
	GB_BA1:PFFC2	5588	Y11998	P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open reading frames.	Pseudomonas fluorescens	63,539	11-Jul-97
rx02414 870	GB_PR4:AC007102	176258	AC007102	Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence.	Homo sapiens	35,069	2-Jun-99
	GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
	GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
rx02435 681	GB_BA2:AF101055	7457	AF101055	Clostridium acetobutylicum atp operon, complete sequence.	Clostridium acetobutylicum	39,605	03-MAR-1999
	GB_OM:RABPKA	4441	J03247	Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds.	Oryctolagus cuniculus	36,061	27-Apr-93
	GB_OM:RABPLASISM	4458	M84656	Oryctolagus cuniculus phosphorylase kinase alpha subunit mRNA, complete cds.	Oryctolagus cuniculus	36,000	22-Jun-98
rx02440 963	GB_EST14:AA417723	374	AA417723	zV01b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746207 3' similar to contains Alu repetitive element; contains element L1 repetitive element.; mRNA sequence.	Homo sapiens	38,770	16-OCT-1997
	GB_EST11:AA215428	303	AA215428	zr95a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683412 3' similar to contains Alu repetitive element.; mRNA sequence.	Homo sapiens	39,934	13-Aug-97
	GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,889	18-Jun-98
rx02453 876	GB_EST14:AA426336	375	AA426336	zv53g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757394 3' mRNA sequence.	Homo sapiens	38,043	16-OCT-1997
	GB_BA1:STMAACC8	1353	M55426	S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds.	Streptomyces fradiae	37,097	05-MAY-1993
	GB_PR3:AC004500	77538	AC004500	Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.	Homo sapiens	33,256	30-MAR-1998
rx02474 897	GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2,3-butanediol dehydrogenase, complete cds.	Brevibacterium saccharolyticum	96,990	13-Feb-99
	GB_OM:BTU71200	877	U71200	Bos taurus acetoin reductase mRNA, complete cds.	Bos taurus	51,659	8-Oct-97
	GB_EST2:F12685	287	F12685	HSC3DA031 normalized infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence	Homo sapiens	41,509	14-Mar-95
rx02480 1779	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,737	23-Jun-99

Table 4 (continued)

rx02485	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,511	24-MAR-1999
	GB_BA1:AP000060	347800	AP000060	Aeropyrum pernix genomic DNA, section 3/7.	Aeropyrum pernix	48,014	22-Jun-99
rx02492 840	GB_BA1:STMPGM	921	M83661	Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds.	Streptomyces coelicolor	65,672	26-Apr-93
	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	61,436	17-Jun-98
	GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	37,893	01-MAR-1994
	GB_PR2:HS161N10	56075	AL008707	Human DNA sequence from PAC 161N10 on chromosome Xq25. Contains EST.	Homo sapiens	37,051	23-Nov-99
rx02528 1098	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98	Drosophila melanogaster	36,822	2-Aug-99
	GB_HTG2:AC008235	136017	AC008235	15.B.19 map 94F-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
	GB_HTG2:AC008235	136017	AC008235	15.B.19 map 94F-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
	GB_BA2:RSU17129	17425	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes.	Rhodococcus erythropolis	66,117	16-Jul-99
rx02539 1641	GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	65,174	17-Jun-98
	GB_BA2:AF068264	3152	AF068264	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds.	Pseudomonas aeruginosa	65,448	18-MAR-1999
	GB_BA1:BACHYPTP	17057	D29985	Bacillus subtilis wapA and orf genes for wall-associated protein and hypothetical proteins.	Bacillus subtilis	53,602	7-Feb-99
	GB_BA1:BACHUTWAP28954	D31856	D31856	Bacillus subtilis genome containing the hut and wapA loci.	Bacillus subtilis	53,602	7-Feb-99
rx02556 1281	GB_BA1:BSGBGLUC	4290	Z34526	B. subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase.	Bacillus subtilis	53,602	3-Jul-95
	GB_HTG3:AC008128	335761	AC008128	Homo sapiens. *** SEQUENCING IN PROGRESS ***. 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	GB_HTG3:AC008128	335761	AC008128	Homo sapiens. *** SEQUENCING IN PROGRESS ***. 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	GB_PL2:AC005292	99053	AC005292	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence.	Arabidopsis thaliana	33,858	16-Apr-99
rx02560 990	GB_JN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	36,420	2-Sep-99
	GB_EST32:A1731605	566	A1731605	BNLGH10201 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004684) hypothetical protein [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,095	11-Jun-99
	GB_JN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	33,707	2-Sep-99

Table 4 (continued)

rx02572 668	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	61,677	17-Jun-98
	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	37,170	17-Jun-98
	GB_HTG1:HS24H01	46989	AL121632	Homo sapiens chromosome 21 clone LLNLc116H0124 map 21q21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	19,820	29-Sep-99
rx02596 1326	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	36,957	24-Jun-99
	GB_BA2:AF026540	1778	AF026540	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	67,627	30-OCT-1998
	GB_BA2:MTU96128	1200	U96128	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	70,417	25-MAR-1998
rx02611 1775	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,532	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	60,575	10-DEC-1996
	GB_BA1:U00014	36470	U00014	Mycobacterium leprae cosmid B1549.	Mycobacterium leprae	57,486	29-Sep-94
rx02612 2316	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,018	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	58,510	10-DEC-1996
	GB_BA1:STMGLEN	2557	L11647	Streptomyces aureofaciens glycogen branching enzyme (glgB) gene, complete cds.	Streptomyces aureofaciens	57,193	25-MAY-1995
rx02621 942	GB_BA1:CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amrR gene and citE gene, partial.	Corynebacterium glutamicum	36,858	12-Aug-99
	GB_IN1:CEM106	39973	Z46935	Caenorhabditis elegans cosmid M106, complete sequence.	Caenorhabditis elegans	37,608	2-Sep-99
	GB_EST29:AI547662	377	AI547662	UI-R-C3-sz-h-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0-UI 3', mRNA sequence.	Rattus norvegicus	50,667	3-Jul-99
rx02640 1650	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	39,187	24-Jun-99
	GB_BA1:PAU49666	4495	U49666	Pseudomonas aeruginosa (orfX), glycerol diffusion facilitator (glpF), glycerol kinase (glpK), and Glp repressor (glpR) genes, complete cds, and (orfK) gene, partial cds.	Pseudomonas aeruginosa	59,273	18-MAY-1997
rx02654 1008	GB_BA1:AB015974	1641	AB015974	Pseudomonas tolaasii glpK gene for glycerol Kinase, complete cds.	Pseudomonas tolaasii	58,339	28-Aug-99
	GB_EST6:N65787	512	N65787	20827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 232B7T7, mRNA sequence.	Arabidopsis thaliana	39,637	5-Jan-98
	GB_PL2:T17H3	65839	AC005916	Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, complete sequence.	Arabidopsis thaliana	33,735	5-Aug-99
	GB_RO:MMU58105	88871	U58105	Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds.	Mus musculus	35,431	13-Feb-97
rx02666 891	GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	38,851	01-MAY-1998

Table 4 (continued)

GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	41,599	01-MAY-1998
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	40,413	1-Jul-98
GB_BA1:PDENQOURF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (URF4), (NQO8), (NQO9), (URF5), (URF6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds; biotin [acetyl-CoA carboxyl] ligase (birA) gene, complete cds.	Paracoccus denitrificans	40,735	20-MAY-1993
GB_BA1:MTCY339	42861	Z77163	Mycobacterium tuberculosis H37Rv complete genome; segment 101/162.	Mycobacterium tuberculosis	36,471	17-Jun-98
GB_BA1:MXADEVRS	2452	L19029	Myxococcus xanthus devR and devS genes, complete cds's.	Myxococcus xanthus	38,477	27-Jan-94
GB_BA1:BACLDH	1147	M19394	B. caldolyticus lactate dehydrogenase (LDH) gene, complete cds.	Bacillus caldolyticus	57,371	26-Apr-93
GB_BA1:BACLDHL	1361	M14788	B. stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	Bacillus stearothermophilus	57,277	26-Apr-93
GB_PAT:A06664	1350	A06664	B. stearothermophilus lct gene.	Bacillus stearothermophilus	57,277	29-Jul-93
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	steatothermophilus Danio rerio	50,746	27-Jun-97
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	36,364	27-Jun-97
GB_EST19:AA758660	233	AA758660	ah67d06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320683 3', mRNA sequence.	Homo sapiens	37,059	29-DEC-1998
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	42,149	27-Jun-97
GB_PR4:AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	37,555	15-Nov-99
GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	99,580	24-Jun-98
GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	38,363	19-Jun-98
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	39,444	27-Jul-98
GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	98,226	24-Jun-98
GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	60,399	12-Jul-99
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	36,426	27-Jul-98
GB_BA1:AB023377	2572	AB023377	Corynebacterium glutamicum tkt gene for transketolase, complete cds.	Corynebacterium glutamicum	99,640	20-Feb-99

Table 4 (continued)

rx02740 1053	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	61,573	04-DEC-1998
	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	61,573	01-MAR-1994
rx02740 1053	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98	Drosophila melanogaster	37,105	2-Aug-99
				48.1.10 map 49E6-49F8 strain y; cn bw sp. *** SEQUENCING IN PROGRESS			
				***, 17 unordered pieces.			
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98	Drosophila melanogaster	37,105	2-Aug-99
rx02741 1089	GB_HTG3:AC007150	121474	AC007150	48.1.10 map 49E6-49F8 strain y; cn bw sp. *** SEQUENCING IN PROGRESS			
				***, 17 unordered pieces.			
				Drosophila melanogaster chromosome 2 clone BACR16P13 (D597) RPCI-98	Drosophila melanogaster	38,728	20-Sep-99
				16.P.13 map 49E-49F strain y; cn bw sp. *** SEQUENCING IN PROGRESS***,			
rx02741 1089	GB_HTG2:AC004951	129429	AC004951	87 unordered pieces.			
				Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***	Homo sapiens	33,116	12-Jun-98
				unordered pieces.			
	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***	Homo sapiens	33,116	12-Jun-98
rx02743 1161	GB_IN1:AB006546	931	AB006546	unordered pieces.			
				Ephydatia fluviatilis mRNA for G protein a subunit 4, partial cds.	Ephydatia fluviatilis	36,379	23-Jun-99
	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	48,401	04-DEC-1998
	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	48,401	01-MAR-1994
rx02797 1026	GB_HTG2:AC007401	83657	AC007401	Homo sapiens clone NH0501007, *** SEQUENCING IN PROGRESS ***	Homo sapiens	37,128	26-Jun-99
				unordered pieces.			
rx02797 1026	GB_BA1:CGBETPGEN	2339	X93514	C. glutamicum betP gene.	Corynebacterium glutamicum	38,889	8-Sep-97
	GB_GSS9:AQ148714	405	AQ148714	HS_3136_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence.	Homo sapiens	34,321	08-OCT-1998
rx02803 680	GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	38,072	1-Feb-97
	GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	34,462	01-MAR-1994
rx02821 363	GB_BA2:PSU85643	4032	U85643	Pseudomonas syringae pv. syringae putative dihydropteroate synthase gene, partial cds, regulatory protein MraA (mraA), triose phosphate isomerase (tpiA), transport protein SecG (secG), tRNA-Leu, tRNA-Met, and 15 kDa protein genes, complete cds.	Pseudomonas syringae pv. syringae	50,445	9-Apr-97
	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	59,314	20-Aug-98
	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***	Homo sapiens	37,607	22-Jul-99
				***, 12 unordered pieces.			
	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***	Homo sapiens	37,607	22-Jul-99
				***, 12 unordered pieces.			
rx02821 363	GB_EST33:AV117143	222	AV117143	AV117143 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone Mus musculus 2610200J17, mRNA sequence.	Mus musculus	40,157	30-Jun-99

Table 4 (continued)

rx02829 373	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
	GB_PR3:HSU85B5	39550	Z69724	Human DNA sequence from cosmid U85B5, between markers DXS366 and DXS87 on chromosome X.	Homo sapiens	41,595	23-Nov-99
rx03216 1141	GB_HTG3:AC008184	151720	AC008184	Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPCI-98 04.D.5 map 36E5-36F2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Drosophila melanogaster	39,600	2-Aug-99
	GB_EST15:AA477537	411	AA477537	zu36g12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 5' similar to contains Alu repetitive element; contains element HGR repetitive element; mRNA sequence.	Homo sapiens	37,260	9-Nov-97
	GB_EST26:AI330662	412	AI330662	fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5', mRNA sequence.	Danio rerio	37,805	28-DEC-1998
rx03215 1038	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor A3(2)	48,657	10-Feb-99
	GB_BA1:SLLINC	36270	X79146	S.lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	39,430	15-MAY-1996
	GB_HTG5:AC009660	204320	AC009660	Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces.	Homo sapiens	35,151	04-DEC-1999
rx03224 1288	GB_PR3:AC004076	41322	AC004076	Homo sapiens chromosome 19, cosmid R30217, complete sequence.	Homo sapiens	37,788	29-Jan-98
	GB_PL2:SPAC926	23193	AL110469	S.pombe chromosome I cosmid c926.	Schizosaccharomyces pombe	38,474	2-Sep-99
	GB_BA2:AE001081	11473	AE001081	Archaeoglobus fulgidus section 26 of 172 of the complete genome.	Archaeoglobus fulgidus	35,871	15-DEC-1997

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7 \text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4 \text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6 \text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6 \text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2 \text{H}_2\text{O}$, 500 mg/l complexing agent
15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by
25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

5

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. et al. (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see e.g., Fleischman, R.D. et al. (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

25

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

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the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g., Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin of replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see e.g., Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described e.g. in Schäfer, A *et al.*

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as
20 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH:
25 Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity
30 to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

- (1988) *Current Protocols in Molecular Biology*, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.
- 10 To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which
- 15 specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

20 **Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions**

- Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der
- 25 Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose,
- 30 ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or
5 ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

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Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

- found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's *Encyclopedia of Industrial Chemistry* (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

- The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

- The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

- The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

- Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 5 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, 10 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

- In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to 15 determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these 20 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- 25 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and 30 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on
5 a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule
10 to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).
15

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. *Ulmann's Encyclopedia of Industrial Chemistry*, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.*
20 (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.
25

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between
30 two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

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90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SMP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SMP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention

were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a
5 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the
10 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP
15 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For
20 example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are
25 well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

• DNA microarrays are solid or flexible supports consisting of nitrocellulose,
30 nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

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may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be
25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g., during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,
30 such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of
5 the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an SMP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an SMP protein involved in the production of a fine chemical.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

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7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

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17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

5 18. An isolated SMP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical.

10

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1,

15

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded
20 by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.

25 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

30

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those

sequences as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

- 5 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 10 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 15 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*,
20 *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*,
Corynebacterium acetophilum, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,
Brevibacterium butanicum, *Brevibacterium divaricatum*, *Brevibacterium flavum*,
Brevibacterium healii, *Brevibacterium ketoglutamicum*, *Brevibacterium*
25 *ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,
Brevibacterium paraffinolyticum, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
- 30 31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

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and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

5 32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine,
10 tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

15

35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 782 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1,
20 thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the
25 Sequence Listing, wherein the nucleic acid molecule is disrupted.

35. 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more
30 nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified
- 5 relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
INVOLVED IN CARBON METABOLISM AND ENERGY
PRODUCTION

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Met Val Asp Val Val
1 5cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc 163
Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln Ala Ala Ser Lys Phe
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Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val
25 30 35gtg ctc acc ggt ggt ggc gcc ggc atc aag ttg ctg gaa aag ctc agc 259
Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser
40 45 50gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc 307
Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly
55 60 65gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag 355
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70 75 80 85gct cgt gag gca ctg ttg tcc aag gtt tct atc cct gaa gcc aac att 403
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90 95 100cac gga tat ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct 451
His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala
105 110 115tac gaa gct gtg ttg gat gaa ttc gca cca aac ggc ttt gat ctt cac 499
Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
120 125 130

ctg ctc ggc atg ggt ggc gaa ggc cat atc aac tcc ctg ttc cct cac 547

Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn Ser Leu Phe Pro His
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 acc gat gca gtc aag gaa tcc tcc gca aag gtc atc gcg gtg ttt gat 595
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 His Ser Ala Lys Arg Val Trp Leu Leu Val Ser Gly Ala Glu Lys Ala
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 20 25 30
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 50 55 60
 His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
 65 70 75 80
 Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile
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 Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
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 Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn
 115 120 125
 Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn
 130 135 140

Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
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Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu
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Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser
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Gly Ala Glu Lys Ala Glu Ala Ala Ala Ile Val Asn Gly Glu Pro
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 Met Ser Lys Thr Ile
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 10 15 20

atc gca gag atg cag gag ctt ccc cca tct gag gct caa ggc ggc gtg 211
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 25 30 35

cag atg tgc aaa atg cag cgc att att gaa cta gca gga act gcc gaa 259
 Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu
 40 45 50

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ctg aat aac gag cca aat gaa gtg gtt ccc cat cca gat acc tat gcg 355
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 70 75 80 85

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 90 95 100

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468

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 35 40 45
 Ala Gly Thr Ala Glu Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly
 50 55 60
 Gly Ser Asn Phe Gln Leu Asn Asn Glu Pro Asn Glu Val Val Pro His
 65 70 75 80
 Pro Asp Thr Tyr Ala Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser
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 gag cag gtg ttg gct gtt cct gat gct gac tgg att cac gtc gac atc 211
 Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp Ile His Val Asp Ile
 25 30 35

atg gac gga cac ttc gtt cca aac ttg agc ttt ggc gcg gat atc aca 259
 Met Asp Gly His Phe Val Pro Asn Leu Ser Phe Gly Ala Asp Ile Thr
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 Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu Asp Val His Leu Met
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atc gaa aac cca gag aag tgg gtg gac aac tac atc gac gct ggc gcg 355
 Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr Ile Asp Ala Gly Ala
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 Asp Cys Ile Val Phe His Val Glu Ala Thr Glu Gly His Val Glu Leu
 90 95 100

gct aag tac atc cgt tcc aag ggt gtg cgt gca ggt ttc tcc ctg cgc 451
 Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala Gly Phe Ser Leu Arg
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cct gga act ccc atc gag gat tac ttg gat gac ctc gag cac ttc gat 499
 Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp Leu Glu His Phe Asp
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gaa gtc atc gtc atg agc gtc gag cct gga ttc ggt ggc caa agc ttc 547
 Glu Val Ile Val Met Ser Val Glu Pro Gly Phe Gly Gly Gln Ser Phe
 135 140 145

atg cct gaa caa ctg gaa aag gtt cgt acc ctg cgc aag gtc atc gat 595
 Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu Arg Lys Val Ile Asp
 150 155 160 165

gag cgc ggt ctg aac acc gtc atc gag atc gac ggc ggc att agc gcc 643
 Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp Gly Gly Ile Ser Ala
 170 175 180

aag acc atc aag cag gct gcc gac gct ggc gtg gat gcc ttc gtt gca 691
 Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val Asp Ala Phe Val Ala
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ggt tcc gct gtg tac ggc gct gag gat ccc aac aag gcg atc cag gag 739
 Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn Lys Ala Ile Gln Glu
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<213> Corynebacterium glutamicum

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 Gly Ala Asp Ile Thr Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu
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 Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr
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 Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu
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 Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala
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 Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp
 115 120 125
 Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe
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 Gly Gly Gln Ser Phe Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu
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 Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp
 165 170 175
 Gly Gly Ile Ser Ala Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val
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 Met Arg Val Tyr Leu
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 gga gca gac cac gct ggt ttc gaa act aaa aat gca atc gca gaa cac 163
 Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn Ala Ile Ala Glu His
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 ctt aag gcc cac ggc cac gaa gtg atc gac tgc gga gcc cac acc tat 211
 Leu Lys Ala His Gly His Glu Val Ile Asp Cys Gly Ala His Thr Tyr

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Thr	Val	Asn	Asp	Pro	Gly	Ser	Leu	Gly	Ile	Val	Leu	Gly	Gly	Ser	Gly					
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Asn	Gly	Glu	Gln	Ile	Ala	Ala	Asn	Lys	Val	Lys	Gly	Ala	Arg	Cys	Ala					
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Leu	Ala	Trp	Ser	Val	Glu	Thr	Ala	Arg	Leu	Ala	Arg	Glu	His	Asn	Asn					
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gcg	aac	ctc	atc	ggc	atc	ggc	ggc	cgc	atg	cac	tca	gag				442				
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 35 40 45
 Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val
 50 55 60
 Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys
 65 70 75 80
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 Ser Glu

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 Met Ser Thr His Ser
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gaa acc acc cgc cca gag ttc atc cac cca gtc tca gtc ctc cca gag 163
 Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu
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gtc tca gct ggt acg gtc ctt gac gct gca gag cca gca ggc gtt ccc 211
 Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro
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acc aaa gat atg tgg gaa tac caa aaa gac cac atg aac ctg gtc tcc 259
 Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His Met Asn Leu Val Ser
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cca ctg aac cga cgc aag ttc cgt gtc ctc gtc gtt ggc acc ggc ctg 307
 Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu
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tcc ggt ggt gct gca gca gca gcc ctc ggc gaa ctc gga tac gac gtc 355
 Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu Leu Gly Tyr Asp Val
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aag gcg ttc acc tac cac gac gca cct cgc cgt gcg cac tcc att gct 403
 Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala
 90 95 100

gca cag ggt ggc gtt aac tcc gcc cgc ggc aag aag gta gac aac gac 451
 Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys Lys Val Asp Asn Asp
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ggc gca tac cgc cac gtc aag gac acc gtc aag ggc ggc gac tac cgt 499
 Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys Gly Gly Asp Tyr Arg
 120 125 130

ggt cgc gag tcc gac tgc tgg cgt ctc gcc gtc gag tcc gtc cgc gtc 547
 Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val
 135 140 145

atc gac cac atg aac gcc atc ggt gca cca ttc gcc cgc gaa tac ggt 595
 Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe Ala Arg Glu Tyr Gly
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ggc gcc ttg gca acc cgt tcc ttc ggt ggt gtg cag gtc tcc cgt acc 643
 Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val Gln Val Ser Arg Thr
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tac tac acc cgt gga caa acc gga cag cag ctg.cag ttc tcc acc gca 691
 Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala
 185 190 195

tcc gca cta cag cgc cag atc cac ctc ggc tcc gta gaa atc ttc acc 739
 Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser Val Glu Ile Phe Thr
 200 205 210

cat aac gaa atg gtt gac gtc att gtc acc gaa cgt aac ggt gaa aag	787
His Asn Glu Met Val Asp Val Ile Val Thr Glu Arg Asn Gly Glu Lys	
215 220 225	
cgc tgc gaa ggc ctg atc atg cgc aac ctg atc acc ggc gag ctc acc	835
Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr	
230 235 240 245	
gca cac acc ggc cat gcc gtt atc ctg gca acc ggt ggc tac ggc aac	883
Ala His Thr Gly His Ala Val Ile Leu Ala Thr Gly Gly Tyr Gly Asn	
250 255 260	
gtg tac cac atg tcc acc ctg gcc aag aac tcc aac gcc tcg gcc atc	931
Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser Asn Ala Ser Ala Ile	
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Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala Ser Pro Ser Phe Ile	
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cag ttc cac cca acc ggc ctg cct gtg aac tcc acc tgg cag tcc aag	1027
Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser Thr Trp Gln Ser Lys	
295 300 305	
acc att ctg atg tcc gag tcg ctg cgt aac gac ggc cgc atc tgg tcc	1075
Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser	
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Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp	
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Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu	
345 350 355	
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Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala	
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ggt ctc ggt gtt gga cct ctg aac aac gct gca tac ctg gac ttc cgc	1267
Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg	
375 380 385	
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Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser	
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Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser	
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Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu	
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Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala	
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 Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn
 455 460 465

tcc ctg ctc tcc gct tcc gtc gat ggc tgg ttc acc ctg cca ttc acc 1555
 Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr
 470 475 480 485

atc cct aac tac ctc ggc cca ttg ctt ggc tcc gag cgt ctg tca gag 1603
 Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu
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gat gca cca gaa gca cag gca gcg att gcg cgt gca cag gct cgc att 1651
 Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile
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gac cgc ctc atg ggc aac cgc cca gag tgg gtc ggt gac aac gtt cac 1699
 Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His
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gga cct gag tac tac cac cgc cag ctt ggc gat atc ctg tac ttc tcc 1747
 Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser
 535 540 545

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 Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys
 550 555 560 565

atc cgt gcc ctc cgc gat gac ttc tgg aag aac atg cgc atc acc ggc 1843
 Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly
 570 575 580

agc acc gat gag atg aac cag gtt ctc gaa tac gca gca cgc gta gcc 1891
 Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala
 585 590 595

gac tac atc gac ctc ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc 1939
 Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg
 600 605 610

gac gag tcc tgt ggc gct cac ttc cgc gac gac cac ctc tcc gaa gat 1987
 Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp His Leu Ser Glu Asp
 615 620 625

ggc gaa gca caa cgt gac gac caa aac tgg tgc ttc gtc tcc gca tgg 2035
 Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp
 630 635 640 645

gaa cca ggc gag aat gga acc ttc gtc tgc cac gca gaa cca ctg ttc 2083
 Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe
 650 655 660

ttc gaa tct gtc cca ctg cag aca agg aac tac aag taatgaaact 2129
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 665 670

tacacttgag atc 2142

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atc cca gtg atg gct cgc aac gtg ctt gag tcc gct cgc ctg ctg gct 1219
 Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser Ala Arg Leu Leu Ala
 360 365 370

aac act tcc cgc gtg ttc gca acc cgt ctc gtt gat ggc att gag cca 1267
 Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val Asp Gly Ile Glu Pro
 375 380 385

aac gag gca cac atg aag gag ctc gct gag tct tca cct tcc atc gtt 1315
 Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser Ser Pro Ser Ile Val
 390 395 400 405

acc cca ctg aac tct gca atc ggc tac gaa gct gct gca aag gtg gct 1363
 Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala Ala Ala Lys Val Ala
 410 415 420

aag act gct ttg gct gag ggc aag acc atc cgc cag act gtc atc gat 1411
 Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg Gln Thr Val Ile Asp
 425 430 435

ttg ggc ttg gtt gat ggc gag aag ctc acc gag gaa gag ctg gac aag 1459
 Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu Glu Glu Leu Asp Lys
 440 445 450

cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc 1507
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<213> Corynebacterium glutamicum

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Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg
 35 40 45

Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser
 50 55 60

Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys
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Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe
 85 90 95

Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile

90										95					100					
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gct	aac	ggc	gtt	gag	gtt	cac	cca	aat	gac	cac	gtc	aac	atg	ggg	cag	499				
Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Gly	Gln					
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tcc	tcc	aat	gac	acc	ttc	cct	act	gca	act	cac	gtt	gct	gca	acc	gaa	547				
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Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val	Val	Lys	Ser	Gly	Arg					
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Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Gly					
			185				190						195							
ggc	tac	gct	cgc	cag	atc	cag	ctc	ggc	atc	gag	cgc	gtt	gag	gct	act	739				
Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu	Arg	Val	Glu	Ala	Thr					
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ctt	cct	cgc	ctt	ggg	gag	ctg	gct	att	ggg	ggc	acc	gct	gct	ggg	acc	787				
Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	Thr	Ala	Ala	Gly	Thr					
		215				220					225									
ggg	atc	aac	acc	tcc	gct	gat	ttc	ggc	ggc	aag	gtt	gtt	gct	gaa	ctg	835				
Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	Val	Val	Ala	Glu	Leu					
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Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	Ala	Glu	Asn	His	Phe					
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Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	Phe	Ser	Gly	Ala	Met					
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cgc	gtt	atc	gct	gtc	tcc	ttg	tac	aag	atc	gct	aac	gat	atc	cgc	ctc	979				
Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu					
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atg	ggc	tcc	ggc	cca	ctg	acc	ggg	ctt	ggc	gag	atc	cgt	ctc	cca	gac	1027				
Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu	Ile	Arg	Leu	Pro	Asp					
		295				300					305									
ctg	cag	cca	ggg	tcc	tcc	atc	atg	cca	ggc	aag	gtc	aac	cca	gtt	ctc	1075				
Leu	Gln	Pro	Gly	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Leu						
310					315					320				325						
tgt	gag	acc	gct	acc	cag	gtt	tcc	gct	cag	gtt	atc	ggc	aat	gac	gca	1123				
Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val	Ile	Gly	Asn	Asp	Ala					
				330					335					340						

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
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Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
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Arg Ala Ala Phe Arg Gly Lys Asp Asp
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 <212> DNA
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<220>
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 <222> (101)..(1507)
 <223> RXA01535

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 Met Thr Glu Gln Glu
 1 5

ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag 163
 Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
 10 15 20

gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc 211
 Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
 25 30 35

tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg 259
 Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
 40 45 50

aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca 307
 Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
 55 60 65

gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt 355
 Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly
 70 75 80 85

aag cat gac gct gag ttc cca att gat gtg ttc cag act ggt tcc ggt 403
 Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly

Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
 150 155 160 165

gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag 643
 Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
 170 175 180

ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg 691
 Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
 185 190 195

cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc 739
 Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
 200 205 210

tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg 787
 Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
 215 220 225

acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga 835
 Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
 230 235 240 245

ggc aaa gac gac tagtctttaa tccaagtaag tac 870
 Gly Lys Asp Asp

<210> 16

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
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Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
 35 40 45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
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Tyr Ile Gly Ile Arg Asp Pro Tyr Ala Gly
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(847)

<223> RXA01311

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 Met Lys Leu Thr Leu
 1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
 10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
 25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
 40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
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gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
 70 75 80 85

cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca 403
 Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
 90 95 100

ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc 451
 Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
 105 110 115

tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac 499
 Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
 120 125 130

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc 547
 Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
 135 140 145

gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt 595

Thr Ala Leu Lys Pro Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn
 145 150 155 160
 Phe Pro Leu Ala Met Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala
 165 170 175
 Gly Cys Val Met Val Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser
 180 185 190
 Gln Tyr Phe Ala Gln Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val
 195 200 205
 Leu Asn Val Val Ser Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile
 210 215 220
 Met Glu Asp Asp Arg Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro
 225 230 235 240
 Val Gly Gln Gln Leu Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr
 245 250 255
 Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala
 260 265 270
 Asp Leu Asp Leu Ala Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn
 275 280 285
 Ile Gly Glu Ala Cys Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser
 290 295 300
 Val Ala Asp Glu Phe Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln
 305 310 315 320
 Val Leu Gly Asn Gly Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val
 325 330 335
 Glu Glu Lys Ala Arg Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val
 340 345 350
 Ala Glu Gly Ala Thr Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala
 355 360 365
 Gly Tyr Phe Tyr Glu Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala
 370 375 380
 Ala Ile Leu Asn Glu Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr
 385 390 395 400
 Phe Gln Thr Glu Glu Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr
 405 410 415
 Gly Leu Ala Ser Tyr Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg
 420 425 430
 Val Ser Asp Gly Leu Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val
 435 440 445
 Ile Ser Asn Ala Ala Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met
 450 455 460

gag atc ttc ggt ccc gtc gca ccg atc gtc acc ttc caa acc gag gaa 1315
 Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr Phe Gln Thr Glu Glu
 390 395 400 405

 gaa gcc ctg cgt cta gcc aac tcc acc gaa tac gga ctg gcc tcc tat 1363
 Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr Gly Leu Ala Ser Tyr
 410 415 420

 gtg ttc acc cag gac acc tca cgt att ttc cgc gtc tcc gat ggt ctc 1411
 Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg Val Ser Asp Gly Leu
 425 430 435

 gag ttc ggc cta gtg ggc gtc aat tcc ggt gtc atc tct aac gct gct 1459
 Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val Ile Ser Asn Ala Ala
 440 445 450

 gca cct ttt ggt ggc gta aaa caa tcc gga atg ggc cgc gaa ggt ggt 1507
 Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met Gly Arg Glu Gly Gly
 455 460 465

 ctc gaa gga atc gag gag tac acc tcc gtg cag tac atc ggt atc cgg 1555
 Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln Tyr Ile Gly Ile Arg
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 Asp Pro Tyr Ala Gly
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 <213> Corynebacterium glutamicum

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 35 40 45

 Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln
 50 55 60

 Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg
 65 70 75 80

 Arg Gly Phe Glu Leu Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu
 85 90 95

 Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val
 100 105 110

 Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg
 115 120 125

 Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu
 130 135 140

gtt ggc ccg tgc ctc ctg atc acc cca tgg aac ttc cca cta gca atg	595
Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn Phe Pro Leu Ala Met	
150 155 160 165	
gct acc cgc aag gtc gca cct gcg atc gct gca ggt tgt gtc atg gtg	643
Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala Gly Cys Val Met Val	
170 175 180	
ctc aag cca gct cga ctt acc ccg ctg acc tcc cag tat ttt gct cag	691
Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser Gln Tyr Phe Ala Gln	
185 190 195	
acc atg ctt gat gcc ggt ctt cca gca ggt gtc ctc aat gtg gtc tcc	739
Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val Leu Asn Val Val Ser	
200 205 210	
ggt gct tcc gcc tct gcg att tcc aac ccg att atg gaa gac gat cgc	787
Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile Met Glu Asp Asp Arg	
215 220 225	
ctt cgt aaa gtc tcc ttc acc ggc tcc acc cca gtt ggc cag cag ctg	835
Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro Val Gly Gln Gln Leu	
230 235 240 245	
ctc aaa aag gct gcc gat aaa gtt ctg cgc acc tcc atg gaa ctt ggt	883
Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr Ser Met Glu Leu Gly	
250 255 260	
ggc aac gca cct ttc att gtc ttc gag gac gcc gac cta gat ctc gcg	931
Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Leu Asp Leu Ala	
265 270 275	
atc gaa ggt gcc atg ggt gcc aaa atg cgc aac atc ggc gaa gct tgc	979
Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys	
280 285 290	
acc gca gcc aac cgt ttc tta gtc cac gaa tcc gtc gcc gat gaa ttc	1027
Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Asp Glu Phe	
295 300 305	
ggc cgt cgc ttc gct gcc cgc ctt gaa gag caa gtc cta ggc aac ggc	1075
Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln Val Leu Gly Asn Gly	
310 315 320 325	
ctc gac gaa ggc gtc acc gtg ggc ccc ctg gtt gag gaa aaa gca cga	1123
Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val Glu Glu Lys Ala Arg	
330 335 340	
gac agc gtt gca tcg ctt gtc gac gcc gcc gtc gcc gaa ggt gcc acc	1171
Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val Ala Glu Gly Ala Thr	
345 350 355	
gtc ctc acc ggc ggc aag gcc ggc aca ggt gca ggc tac ttc tac gaa	1219
Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala Gly Tyr Phe Tyr Glu	
360 365 370	
cca acg gtg ctc acg gga gtt tca aca gat gcg gct atc ctg aac gaa	1267
Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala Ala Ile Leu Asn Glu	
375 380 385	

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					Met	Thr	Ile	Asn	Val							
									1					5		
ttc	gaa	cta	ctt	gtc	aaa	agt	ccc	acg	ggc	cta	ctg	att	ggc	gat	tcc	163
Phe	Glu	Leu	Leu	Val	Lys	Ser	Pro	Thr	Gly	Leu	Leu	Ile	Gly	Asp	Ser	
				10					15					20		
tgg	gtg	gaa	gca	tcc	gac	ggc	ggc	act	ttc	gat	gtg	gaa	aac	cca	gcg	211
Trp	Val	Glu	Ala	Ser	Asp	Gly	Gly	Thr	Phe	Asp	Val	Glu	Asn	Pro	Ala	
			25					30					35			
acg	ggc	gaa	aca	atc	gca	acg	ctc	gcg	tct	gct	act	tcc	gag	gat	gca	259
Thr	Gly	Glu	Thr	Ile	Ala	Thr	Leu	Ala	Ser	Ala	Thr	Ser	Glu	Asp	Ala	
		40					45					50				
ctg	gct	gct	ctt	gat	gct	gca	tgc	gct	gtt	cag	gcc	gag	tgg	gct	agg	307
Leu	Ala	Ala	Leu	Asp	Ala	Ala	Cys	Ala	Val	Gln	Ala	Glu	Trp	Ala	Arg	
		55				60					65					
atg	cca	gcg	cgc	gag	cgt	tct	aat	att	tta	cgc	cgc	ggc	ttt	gag	ctc	355
Met	Pro	Ala	Arg	Glu	Arg	Ser	Asn	Ile	Leu	Arg	Arg	Gly	Phe	Glu	Leu	
	70				75					80					85	
gta	gca	gaa	cgt	gca	gaa	gag	ttc	gcc	acc	ctc	atg	acc	ttg	gaa	atg	403
Val	Ala	Glu	Arg	Ala	Glu	Glu	Phe	Ala	Thr	Leu	Met	Thr	Leu	Glu	Met	
				90					95					100		
ggc	aag	cct	ttg	gct	gaa	gct	cgc	ggc	gaa	gtc	acc	tac	ggc	aac	gaa	451
Gly	Lys	Pro	Leu	Ala	Glu	Ala	Arg	Gly	Glu	Val	Thr	Tyr	Gly	Asn	Glu	
			105					110					115			
ttc	ctg	cgc	tgg	ttc	tct	gag	gaa	gca	gtt	cgt	ctg	tat	ggc	cgt	tac	499
Phe	Leu	Arg	Trp	Phe	Ser	Glu	Glu	Ala	Val	Arg	Leu	Tyr	Gly	Arg	Tyr	
		120				125						130				
gga	acc	aca	cca	gaa	ggc	aac	ttg	cgg	atg	ctg	acc	gcc	ctc	aag	cca	547
Gly	Thr	Thr	Pro	Glu	Gly	Asn	Leu	Arg	Met	Leu	Thr	Ala	Leu	Lys	Pro	
	135				140						145					

Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn
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 Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe
 20 25 30
 Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val
 35 40 45
 Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly
 50 55 60
 Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg
 65 70 75 80
 Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met
 85 90 95
 Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
 100 105 110
 Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
 115 120 125
 Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp
 130 135 140
 Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala
 145 150 155 160
 Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
 165 170 175
 Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
 180 185 190
 Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
 195 200 205
 Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr
 210 215 220
 His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg
 225 230 235 240
 Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
 245 250 255
 Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
 260 265 270
 Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu
 275 280 285
 Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly
 290 295 300
 Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg
 305 310 315 320
 Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn

145	150	155	160	
tcc gtc gat ggc tgg ttc acc ctg cca ttc acc atc cct aac tac ctg				528
Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu				
	165	170	175	
ggc cca ttg ctt ggc tcc gag cgt ctg tca gag gat gca cca gaa gca				576
Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala				
	180	185	190	
cag gca gcg att gcg cgt gca cag gct cgc att gac cgc ctc atg ggc				624
Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly				
	195	200	205	
aac cgc cca gag tgg gtc ggt gac aac gtt cac gga cct gag tac tac				672
Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr				
	210	215	220	
cac cgc cag ctt ggc gat atc ctg tac ttc tcc tgt ggc gtt tcc cga				720
His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg				
	225	230	235	240
aac gta gaa gac ctc cag gat ggc atc aac aag atc cgt gcc ctc cgc				768
Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg				
	245	250	255	
gat gac ttc tgg aag aac atg cgc atc acc ggc agc acc gat gag atg				816
Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met				
	260	265	270	
aac cag gtt ctc gaa tac gca gca cgc gta gcc gac tac atc gac ctc				864
Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu				
	275	280	285	
ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc gac gag tcc tgt ggc				912
Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly				
	290	295	300	
gct cac ttc cgc gac gac cac ctc tcc gaa gat ggc gaa gca caa cgt				960
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg				
	305	310	315	320
gac gac caa aac tgg tgc ttc gtc tcc gca tgg gaa cca ggc gag aat				1008
Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn				
	325	330	335	
gga acc ttc gtc tgc cac gca gaa cca ctg ttc ttc gaa tct gtc cca				1056
Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro				
	340	345	350	
ctg cag aca agg aac tac aag taatgaaact tacacttgag atc				1100
Leu Gln Thr Arg Asn Tyr Lys				
	355			

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<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

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<211> 1100
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (1)..(1077)
<223> FRXA01312
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1				5				10				15				
gat	aac	cgc	gat	cca	aac	acc	atc	cct	gag	gat	gag	cgc	gac	tac	ttc	96
Asp	Asn	Arg	Asp	Pro	Asn	Thr	Ile	Pro	Glu	Asp	Glu	Arg	Asp	Tyr	Phe	
20				25				30								
ctg	gag	cgc	cgc	tac	cca	gca	ttc	ggc	aac	ctc	gtc	cca	cgt	gac	gtt	144
Leu	Glu	Arg	Arg	Tyr	Pro	Ala	Phe	Gly	Asn	Leu	Val	Pro	Arg	Asp	Val	
35				40				45								
gct	tcc	cgt	gcg	atc	tcc	cag	cag	atc	aat	gct	ggc	ctc	ggc	gtt	gga	192
Ala	Ser	Arg	Ala	Ile	Ser	Gln	Gln	Ile	Asn	Ala	Gly	Leu	Gly	Val	Gly	
50				55				60								
cct	ctg	aac	aac	gct	gca	tac	ctg	gac	ttc	cgc	gac	gcc	acc	gag	cgc	240
Pro	Leu	Asn	Asn	Ala	Ala	Tyr	Leu	Asp	Phe	Arg	Asp	Ala	Thr	Glu	Arg	
65				70				75				80				
ctc	gga	cag	gac	acc	atc	cgc	gag	cgt	tac	tcc	aac	ctc	ttc	acc	atg	288
Leu	Gly	Gln	Asp	Thr	Ile	Arg	Glu	Arg	Tyr	Ser	Asn	Leu	Phe	Thr	Met	
85				90				95								
tac	gaa	gag	gca	att	ggc	gag	gac	cca	tac	tcc	agc	cca	atg	cgt	att	336
Tyr	Glu	Glu	Ala	Ile	Gly	Glu	Asp	Pro	Tyr	Ser	Ser	Pro	Met	Arg	Ile	
100				105				110								
gca	ccg	acc	tgc	cac	ttc	acc	atg	ggc	ggc	ctc	tgg	act	gac	ttc	aac	384
Ala	Pro	Thr	Cys	His	Phe	Thr	Met	Gly	Gly	Leu	Trp	Thr	Asp	Phe	Asn	
115				120				125								
gaa	atg	acg	tca	ctc	cca	ggc	ctg	ttc	tgc	gca	ggc	gaa	gca	tcc	tgg	432
Glu	Met	Thr	Ser	Leu	Pro	Gly	Leu	Phe	Cys	Ala	Gly	Glu	Ala	Ser	Trp	
130				135				140								
acc	tac	cac	ggc	gca	aac	cgt	ctg	ggc	gca	aac	tcc	ctg	ctc	tcc	gct	480
Thr	Tyr	His	Gly	Ala	Asn	Arg	Leu	Gly	Ala	Asn	Ser	Leu	Leu	Ser	Ala	

Thr Trp Gln Ser Lys Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp
 305 310 315 320
 Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn
 325 330 335
 Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro
 340 345 350
 Ala Phe Gly Asn Leu Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser
 355 360 365
 Gln Gln Ile Asn Ala Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala
 370 375 380
 Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile
 385 390 395 400
 Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly
 405 410 415
 Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe
 420 425 430
 Thr Met Gly Gly Leu Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro
 435 440 445
 Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn
 450 455 460
 Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe
 465 470 475 480
 Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser
 485 490 495
 Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg
 500 505 510
 Ala Gln Ala Arg Ile Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val
 515 520 525
 Gly Asp Asn Val His Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp
 530 535 540
 Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln
 545 550 555 560
 Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn
 565 570 575
 Met Arg Ile Thr Gly Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr
 580 585 590
 Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val
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 Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp
 610 615 620
 His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys

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<213> *Corynebacterium glutamicum*

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Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
 35 40 45

Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val
 50 55 60

Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Ala Leu Gly Glu
 65 70 75 80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg
 85 90 95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys
 100 105 110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys
 115 120 125

Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val
 130 135 140

Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe
 145 150 155 160

Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val
 165 170 175

Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu
 180 185 190

Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser
 195 200 205

Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu
 210 215 220

Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile
 225 230 235 240

Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr
 245 250 255

Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser
 260 265 270

Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala
 275 280 285

Ser Pro Ser Phe Ile Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser
 290 295 300

100					105					110					
Ala	Ser	Ile	Ala	Lys	Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His
		115					120					125			
Val	Asn	Met	Gly	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His
		130					135					140			
Val	Ala	Ala	Thr	Glu	Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys
							150					155			160
Val	Leu	His	Glu	Ser	Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val
				165					170					175	
Val	Lys	Ser	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu
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							215					220			
Thr	Ala	Ala	Gly	Thr	Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys
							230					235			240
Val	Val	Ala	Glu	Leu	Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu
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Ala	Glu	Asn	His	Phe	Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu
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Phe	Ser	Gly	Ala	Met	Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala
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Asn	Asp	Ile	Arg	Leu	Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu
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Ala	Arg	Leu	Leu	Ala	Asn	Thr	Ser	Arg	Val	Phe	Ala	Thr	Arg	Leu	Val
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Asp	Gly	Ile	Glu	Pro	Asn	Glu	Ala	His	Met	Lys	Glu	Leu	Ala	Glu	Ser
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Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
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<223> RXA00517

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 Met Pro Glu Val Thr
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gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa 163
 Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys
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act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg 211
 Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val
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cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct 259
 Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro
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 Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His
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 Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His
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 Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val
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 Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser
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Ala	Pro	Phe	Gly	Glu	Thr	Ala	Thr	Val	Val	Asp	Ile	Ala	Asn	Thr	Ala		
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Val	Ala	Arg	Gly	Lys	Ile	Tyr	His	Ala	Arg	Gln	Thr	Asn	Met	Pro	Ile		
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Pro	Glu	Thr	Trp	Ala	Ile	Thr	Ser	Glu	Gly	Ala	Pro	Thr	Thr	Asp	Pro		
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Ala	Glu	Ala	Ile	Asn	Gly	Val	Val	Leu	Pro	Met	Ala	Gly	His	Lys	Gly		
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Tyr	Ala	Ile	Ser	Phe	Met	Met	Asp	Val	Leu	Ser	Gly	Val	Leu	Thr	Gly		
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Ser	Gln	His	Ser	Thr	Lys	Val	His	Gly	Pro	Tyr	Asp	Pro	Thr	Pro	Pro		
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Gly	Gly	Ala	Gly	His	Leu	Phe	Ile	Ala	Leu	Asp	Val	Ala	Ala	Phe	Arg		
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Asp	Pro	Gln	Asp	Phe	Asp	Asp	Ala	Leu	Ser	Asp	Leu	Val	Gly	Glu	Val		
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Leu	Pro	Glu	Lys	Thr	Trp	Met	Glu	Leu	Gln	Glu	Leu	Ala	Ile	Glu	Asn		
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 35 40 45
 Val Leu Arg Leu Pro Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met
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 Thr Thr His Ala His Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu
 65 70 75 80
 Ala Leu Asp Gly His Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala
 85 90 95
 Arg Lys Glu Ala Val Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val
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 Ser Val Arg Asn Ser Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg
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 Lys Ala Ala Ala Gln Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser
 130 135 140
 Pro Ala Met Ala Pro Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn
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 Pro Trp Ser Ile Ala Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp
 165 170 175
 Ile Ala Asn Thr Ala Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln
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 Thr Asn Met Pro Ile Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala
 195 200 205
 Pro Thr Thr Asp Pro Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met
 210 215 220
 Ala Gly His Lys Gly Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser
 225 230 235 240
 Gly Val Leu Thr Gly Ser Gln His Ser Thr Lys Val His Gly Pro Tyr
 245 250 255
 Asp Pro Thr Pro Pro Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp
 260 265 270
 Val Ala Ala Phe Arg Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp
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 Leu Val Gly Glu Val Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu
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 Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser
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 Met Asn Ser Pro Gln
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 aac gtc tcc acc aag aag gtc acc gtc acc ggc gca gct ggt caa atc 163
 Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile
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 Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr
 25 30 35
 gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc 259
 Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly
 40 45 50
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 Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu
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 90 95 100
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 Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val
 120 125 130
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 Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala
 135 140 145
 cca gat gtt cca gca tcc cgc ttc aac gca atg atg cgc ctt gat cac 595

Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His
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 Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala
 170 175 180

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 Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser Ala Thr Gln Phe
 185 190 195

cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg 739
 Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu
 200 205 210

gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac 787
 Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn
 215 220 225

cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct 835
 Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser
 230 235 240 245

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 Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile
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 Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu
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 295 300 305

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225					230					235					240	
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Gly	Ala	Tyr	Gly	Ile	Pro	Glu	Gly	Ile	Phe	Val	Gly	Leu	Pro	Thr	Val	
275					280					285						
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Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn Ser Ala Ala Trp Gly
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Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu
          120          125          130

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Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile
          135          140          145

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Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val
          150          155          160          165

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Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu
          170          175          180

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Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala
          185          190          195

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 gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg 835
 Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu
 230 235 240 245
 ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc 883
 Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile
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 Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg
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 Ile Phe Asp Leu Val Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala
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 Val Gly Leu Ala Val Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val
 65 70 75 80
 Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys
 85 90 95
 Leu Glu Asn Leu Leu Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn
 100 105 110

Ser Ala Ala Trp Gly Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp
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 Asn Trp Val Leu Leu Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile
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 Glu Lys Gly Glu Ile Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe
 145 150 155 160
 Gly His Leu Arg Val Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys
 165 170 175
 Glu Gly Cys Leu Glu Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr
 180 185 190
 Ala Arg Glu Leu Ala Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe
 195 200 205
 Asp Lys Ile Lys Ala Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr
 210 215 220
 Ala Ala Ala Arg Gln Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp
 225 230 235 240
 Phe Ser Glu Trp Leu Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu
 245 250 255
 Asp Pro Gly Met Ile Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp
 260 265 270
 Leu Tyr Leu Asp Arg Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly
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25 30 35	
cag gtc gct ttc ggc acc tcc gga cac cgt ggc ttc gcg ctg gac agc Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser	259
40 45 50	
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55 60 65	
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70 75 80 85	
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90 95 100	
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105 110 115	
tac acc ccg acg ccc gca gtg tcc cac gcg atc cta cga cac aac gat Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp	499
120 125 130	
ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly	547
135 140 145	
atc gtg atc acc cca tcc cac aac cct cct cgt gat ggc gga ttc aaa Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys	595
150 155 160 165	
tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp	643
170 175 180	
atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val	691
185 190 195	
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200 205 210	
gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile	787
215 220 225	
gat gcc atc cgc gaa gct ggt gtt cga atc ggc gca gac cca atg ggt Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly	835
230 235 240 245	
ggc gca tcc gtg gat tac tgg ggt gcc atc gca gaa acc cat ggc ctc	883

Gly	Ala	Ser	Val	Asp	Tyr	Trp	Gly	Ala	Ile	Ala	Glu	Thr	His	Gly	Leu	
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aac	ctc	acc	gtg	gtc	aac	cca	cac	gtt	gat	tcc	acc	ttc	cgc	ttc	atg	931
Asn	Leu	Thr	Val	Val	Asn	Pro	His	Val	Asp	Ser	Thr	Phe	Arg	Phe	Met	
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Thr	Leu	Asp	Thr	Asp	Gly	Lys	Ile	Arg	Met	Asp	Cys	Ser	Ser	Pro	His	
		280					285					290				
gca	atg	gca	tcg	ctg	att	gac	aac	cga	gac	aag	ttc	gat	gtg	gca	acc	1027
Ala	Met	Ala	Ser	Leu	Ile	Asp	Asn	Arg	Asp	Lys	Phe	Asp	Val	Ala	Thr	
	295					300					305					
ggc	aac	gac	gcc	gac	gcc	gac	cgc	cac	ggc	atc	gtc	acc	cca	gac	gct	1075
Gly	Asn	Asp	Ala	Asp	Ala	Asp	Arg	His	Gly	Ile	Val	Thr	Pro	Asp	Ala	
310					315					320					325	
ggc	ttg	atg	aac	ccc	aac	cac	tac	ctc	gca	gta	gca	att	gag	tac	ctc	1123
Gly	Leu	Met	Asn	Pro	Asn	His	Tyr	Leu	Ala	Val	Ala	Ile	Glu	Tyr	Leu	
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ttt	gct	cac	cgc	cca	ggc	tgg	tcc	gca	gat	acc	gca	gtg	ggc	aaa	acc	1171
Phe	Ala	His	Arg	Pro	Gly	Trp	Ser	Ala	Asp	Thr	Ala	Val	Gly	Lys	Thr	
			345					350					355			
ctg	gtc	agc	tcc	tcc	atg	atc	gac	cgc	gtt	gtg	gcg	cag	ctt	ggc	cgc	1219
Leu	Val	Ser	Ser	Ser	Met	Ile	Asp	Arg	Val	Val	Ala	Gln	Leu	Gly	Arg	
		360					365					370				
acc	ctc	gtt	gag	gtt	cca	gtc	gga	ttc	aag	tgg	ttt	gtc	cca	ggc	ttg	1267
Thr	Leu	Val	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp	Phe	Val	Pro	Gly	Leu	
	375					380					385					
atc	tcc	ggc	gaa	atc	gga	ttc	ggc	ggc	gaa	gaa	tcc	gca	ggc	gca	tcc	1315
Ile	Ser	Gly	Glu	Ile	Gly	Phe	Gly	Gly	Glu	Glu	Ser	Ala	Gly	Ala	Ser	
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ttc	ctc	cgc	atg	gac	ggc	acc	acc	tgg	tcc	acc	gac	aag	gac	ggc	ctc	1363
Phe	Leu	Arg	Met	Asp	Gly	Thr	Thr	Trp	Ser	Thr	Asp	Lys	Asp	Gly	Leu	
				410					415					420		
atc	ctt	gac	ctc	ctg	gca	gct	gag	atc	att	gca	gta	acc	ggc	aag	acc	1411
Ile	Leu	Asp	Leu	Leu	Ala	Ala	Glu	Ile	Ile	Ala	Val	Thr	Gly	Lys	Thr	
			425					430					435			
cca	tca	cag	cgc	tac	gca	gaa	ctc	gcc	gaa	gaa	ttc	ggc	gca	cct	gcc	1459
Pro	Ser	Gln	Arg	Tyr	Ala	Glu	Leu	Ala	Glu	Glu	Phe	Gly	Ala	Pro	Ala	
		440					445					450				
tac	gcc	cgc	acc	gat	gca	gaa	gcc	aac	cga	gaa	caa	aag	gcc	atc	ctg	1507
Tyr	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Asn	Arg	Glu	Gln	Lys	Ala	Ile	Leu	
	455					460					465					
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Lys	Ala	Leu	Ser	Pro	Glu	Gln	Val	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Glu	
470					475					480					485	
gca	atc	acc	gct	aag	ctc	acc	gaa	gct	ccc	ggc	aat	ggc	gca	gcc	atc	1603
Ala	Ile	Thr	Ala	Lys	Leu	Thr	Glu	Ala	Pro	Gly	Asn	Gly	Ala	Ala	Ile	

490	495	500	
gga gga cta aaa gtg acc acc gaa aac gcc tgg ttc gca gca cgc cca			1651
Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp Phe Ala Ala Arg Pro			
505	510	515	
tcc ggc acc gaa gac aag tac aag atc tac gca gaa tcc ttc aag ggc			1699
Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala Glu Ser Phe Lys Gly			
520	525	530	
gaa gag cac ctc gcc cag gtt cag aag gaa gcc caa gcg ttg gtc agc			1747
Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala Gln Ala Leu Val Ser			
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Glu Val Leu Gly Gln			
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<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

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Asn	Asn	Pro	Asp	Gln	Gln	Val	Ala	Phe	Gly	Thr	Ser	Gly	His	Arg	Gly
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Phe	Ala	Leu	Asp	Ser	Ala	Phe	Asn	Glu	Asp	His	Ile	Leu	Ala	Thr	Thr
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Gln	Ala	Ile	Val	Asp	Tyr	Arg	Asn	Gln	Gln	Pro	Lys	Asn	Trp	Val	Gly
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Pro	Leu	Phe	Ile	Gly	Arg	Asp	Thr	His	Ala	Leu	Ser	Glu	Pro	Ala	Met
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Ile	Ser	Ala	Leu	Glu	Val	Leu	Ile	Ala	Asn	Asp	Val	Glu	Val	Leu	Val
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Asp	Ala	Asp	Gly	Arg	Tyr	Thr	Pro	Thr	Pro	Ala	Val	Ser	His	Ala	Ile
		115					120					125			

Leu	Arg	His	Asn	Asp	Gly	Ile	Ile	Leu	Gly	Thr	Ala	Gly	Pro	Ser	Arg
130						135					140				

Pro	Tyr	Ala	Asp	Gly	Ile	Val	Ile	Thr	Pro	Ser	His	Asn	Pro	Pro	Arg
145					150					155					160

Asp	Gly	Gly	Phe	Lys	Tyr	Asn	Pro	Ala	Asn	Gly	Gly	Pro	Ala	Asp	Thr
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Asp	Ala	Thr	Asp	Trp	Ile	Ala	Asn	Arg	Ala	Asn	Asp	Ile	Leu	Arg	Gly
			180					185					190		

Asp Leu Ala Asp Val Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu
 195 200 205
 Arg Thr Thr Ala Tyr Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro
 210 215 220
 Asn Val Val Asn Ile Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly
 225 230 235 240
 Ala Asp Pro Met Gly Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala
 245 250 255
 Glu Thr His Gly Leu Asn Leu Thr Val Val Asn Pro His Val Asp Ser
 260 265 270
 Thr Phe Arg Phe Met Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp
 275 280 285
 Cys Ser Ser Pro His Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys
 290 295 300
 Phe Asp Val Ala Thr Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile
 305 310 315 320
 Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val
 325 330 335
 Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr
 340 345 350
 Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val
 355 360 365
 Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp
 370 375 380
 Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu
 385 390 395 400
 Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr
 405 410 415
 Asp Lys Asp Gly Leu Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala
 420 425 430
 Val Thr Gly Lys Thr Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu
 435 440 445
 Phe Gly Ala Pro Ala Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu
 450 455 460
 Gln Lys Ala Ile Leu Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr
 465 470 475 480
 Glu Leu Ala Gly Glu Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly
 485 490 495
 Asn Gly Ala Ala Ile Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp
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 Phe Ala Ala Arg Pro Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala

515					520					525						
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Gln Ala Leu Val Ser					Glu Val Leu Gly Gln											
545					550											
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Val	Ser	Gly	Glu	Met	Leu	Ala	Ala	Ala	Leu	Ser	Ala	Gly	Met	Ala	Ser	
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Gln	Gly	Val	Asp	Val	Ile	Arg	Val	Gly	Val	Ile	Pro	Thr	Pro	Ala	Val	
			20					25					30			
gca	ttc	ctc	acc	gat	gat	tat	ggc	gct	gac	atg	ggc	gtg	atg	att	tct	144
Ala	Phe	Leu	Thr	Asp	Asp	Tyr	Gly	Ala	Asp	Met	Gly	Val	Met	Ile	Ser	
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Ala	Ser	His	Asn	Pro	Met	Pro	Asp	Asn	Gly	Ile	Lys	Phe	Phe	Ser	Ala	
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Gly	Gly	His	Lys	Leu	Pro	Asp	His	Val	Glu	Asp	Glu	Ile	Glu	Arg	Val	
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Met	Asp	Ser	Leu	Pro	Ala	Glu	Gly	Pro	Thr	Gly	His	Gly	Val	Gly	Arg	
				85				90						95		
gtc	atc	gaa	gaa	gca	acc	gat	gca	cag	gac	cgt	tac	cta	gag	cac	ctg	336
Val	Ile	Glu	Glu	Ala	Thr	Asp	Ala	Gln	Asp	Arg	Tyr	Leu	Glu	His	Leu	
			100					105					110			
aag	gaa	gct	gtt	cct	acg	tca	ctt	gaa	ggc	atc	aag	att	gtt	gtg	gat	384
Lys	Glu	Ala	Val	Pro	Thr	Ser	Leu	Glu	Gly	Ile	Lys	Ile	Val	Val	Asp	
		115					120					125				
gca	gcc	aat	ggt	gcg	gca	agt	gtt	gta	gct	cca	acg	gct	tat	gag	gct	432
Ala	Ala	Asn	Gly	Ala	Ala	Ser	Val	Val	Ala	Pro	Thr	Ala	Tyr	Glu	Ala	
	130					135					140					
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Ala	Gly	Ala	Thr	Val	Ile	Ala	Ile	His	Asn	Lys	Pro	Asp	Ser	Tyr	Asn	
145				150						155					160	
atc	aac	atg	gac	tgc	ggt	tcc	acc	cac	att	gat	cag	gcg	cag	ccg	cca	528

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Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
      180                      185                      190

gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac 624
Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp
      195                      200                      205

caa atc atg gcg ctg tta gcc att gcg atg aaa taaaacggcg agctgcgcaa 677
Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys
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gaa 680

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      20          25          30

Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
      35          40          45

Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
      50          55          60

Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
      65          70          75          80

Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
      85          90          95

Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
      100          105          110

Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
      115          120          125

Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
      130          135          140

Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
      145          150          155          160

Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
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Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
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Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp

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Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala
20 25 30

ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct gca 144
Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
35 40 45

tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt 192
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
50 55 60

gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg 240
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
65 70 75 80

gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc 288
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
85 90 95

atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag 336
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
100 105 110

gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca 384
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
115 120 125

gcc aat ggt gcg gca 399
Ala Asn Gly Ala Ala
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<210> 30
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Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly	50	55	60
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met	65	70	75
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val	85	90	95
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys	100	105	110
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala	115	120	125
Ala Asn Gly Ala Ala	130		

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 <223> RXN03076

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 Met Asp Glu Ser Arg
 1 5
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 Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
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 cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt 211
 Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
 25 30 35
 gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259
 Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
 40 45 50
 gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat 307
 Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
 55 60 65
 ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat 355

Gly	Pro	Leu	Arg	Val	Val	Val	Gly	Tyr	Asp	Ala	Arg	Tyr	Gly	Ser	His	
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Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala	Gly	Ala	Gly	Phe	Glu	
				90					95					100		
gtg	acg	ttg	ctc	ccc	acg	cct	agc	cct	acg	ccg	ttg	att	ccg	tgg	ttg	451
Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro	Leu	Ile	Pro	Trp	Leu	
			105					110					115			
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Val	Asn	Lys	His	Gly	Leu	Asp	Ala	Gly	Val	Gln	Ile	Thr	Ala	Ser	His	
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aat	ggg	gcg	gcg	gac	aat	ggc	tac	aag	gtg	ttt	ttg	tct	aat	ggt	cgc	547
Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe	Leu	Ser	Asn	Gly	Arg	
	135					140					145					
cag	ctt	tat	tct	gaa	ctg	gag	cct	gag	ctt	gag	gcg	cat	atc	aat	gct	595
Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu	Ala	His	Ile	Asn	Ala	
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Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr	Val	Arg	Pro	Thr	Ala	
				170				175						180		
gat	cag	ctg	cgt	cga	tat	gtt	gat	gag	atg	gtg	tcg	ttg	gtg	act	cct	691
Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val	Ser	Leu	Val	Thr	Pro	
			185					190					195			
gat	cag	gct	gat	ttg	ttg	cgg	gtg	aat	tct	gag	cgg	ggc	aat	ctt	cgc	739
Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu	Arg	Gly	Asn	Leu	Arg	
		200					205					210				
gtg	gtg	tat	acc	gct	ctg	cat	ggg	gtg	ggg	ggc	cgc	gcg	atg	gcc	aat	787
Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly	Arg	Ala	Met	Ala	Asn	
	215					220					225					
gct	ttc	caa	ttt	gct	ggg	ttt	ccc	cat	act	cat	ggc	gtg	aag	gct	cag	835
Ala	Phe	Gln	Phe	Ala	Gly	Phe	Pro	His	Thr	His	Gly	Val	Lys	Ala	Gln	
	230				235					240					245	
cag	tat	cct	gat	ccc	acc	ttc	ccc	act	gtg	gcg	ttc	ccc	aat	ccg	gaa	883
Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu	
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gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cgc	gca	aag	gaa	aag	aac	931
Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn	
			265					270					275			
gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cgt	tgt	gct	gtg	979
Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val	
		280					285					290				
ggg	att	cgt	acc	gct	gat	ggc	ggc	cac	cga	atg	ctc	tct	ggc	gat	gag	1027
Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	Leu	Ser	Gly	Asp	Glu	
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gtg	ggc	aca	ctt	ttg	gct	act	cgt	ttg	gtt	ccg	gag	tat	tcc	ggt	gaa	1075
Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu	

310	315	320	325	
ggc cca cgt ccc	gtg gtt gcc acc acg	gtg tct tcg cag ctt ctg	1123	
Gly Pro Arg Pro	Val Val Ala Thr Thr	Val Ser Ser Gln Leu Leu		
	330	335	340	
ggt atc atc gcc	gag gat aaa ggg tgg	gat tat tcc gag aca ctg acg	1171	
Gly Ile Ile Ala	Glu Asp Lys Gly Trp	Asp Tyr Ser Glu Thr Leu Thr		
	345	350	355	
gga ttc aaa aat	ctg tcg agg gct gcc	gat ggt ctc gac gga ccg ctt	1219	
Gly Phe Lys Asn	Leu Ser Arg Ala Ala	Asp Gly Pro Leu		
	360	365	370	
gct ttc gct tat	gag gaa gct gtg ggc	acc tgc ccg gtt cca	gat gtc	1267
Ala Phe Ala Tyr	Glu Glu Ala Val Gly	Thr Cys Pro Val Pro	Asp Val	
	375	380	385	
gtg ccg gat aag	gac ggc atc tct aca	gcg ttg ttc atg gcg	tcg tgg	1315
Val Pro Asp Lys	Asp Gly Ile Ser Thr	Ala Leu Phe Met Ala	Ser Trp	
	390	395	400	405
gct gcc gaa ctg	aag gct cag ggc gca	agc ctg cag caa aaa	ctc aat	1363
Ala Ala Glu Leu	Lys Ala Gln Gly Ala	Ser Leu Gln Gln Lys	Leu Asn	
	410	415	420	
gag ttg tat cgc	cga tat ggg tat ttt	gcg tcc tcg caa att	gct gtg	1411
Glu Leu Tyr Arg	Arg Tyr Gly Tyr Phe	Ala Ser Ser Gln Ile	Ala Val	
	425	430	435	
cgc acg agc agt	cca cgc gag tta gtt	gat cac tgg att gcg	cat cct	1459
Arg Thr Ser Ser	Pro Arg Glu Leu Val	Asp His Trp Ile Ala	His Pro	
	440	445	450	
cag caa gaa ctc	att gga gtg tct gtc	acc cca cat att ctt	cct gaa	1507
Gln Gln Glu Leu	Ile Gly Val Ser Val	Thr Pro His Ile Leu	Pro Glu	
	455	460	465	
aaa cag ggc att	gct ttg cat ggc cag	gtg ggg cat gtg cat	atc cgt	1555
Lys Gln Gly Ile	Ala Leu His Gly Gln	Val Gly His Val His	Ile Arg	
	470	475	480	485
gct att ggt cga	gtc tct gga act gag	gcg aaa gcc aag ctc	tat ttg	1603
Ala Ile Gly Arg	Val Ser Gly Thr Glu	Ala Lys Ala Lys Leu	Tyr Leu	
	490	495	500	
gaa gtt ggt cag	gcc agc tcc cat gat	gaa gca gct cag ttg	ttg cat	1651
Glu Val Gly Gln	Ala Ser Ser His Asp	Glu Ala Ala Gln Leu	Leu His	
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cag ctg gag gat	gaa gtc caa agc tgg	ttg agc aag ctt tag	tttcctg	1700
Gln Leu Glu Asp	Glu Val Gln Ser Trp	Leu Ser Lys Leu		
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<210> 32

<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

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 20 25 30
 Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
 35 40 45
 Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
 50 55 60
 Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
 65 70 75 80
 Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
 85 90 95
 Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
 100 105 110
 Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
 115 120 125
 Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
 130 135 140
 Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
 145 150 155 160
 Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
 165 170 175
 Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
 180 185 190
 Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
 195 200 205
 Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
 210 215 220
 Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
 225 230 235 240
 Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
 290 295 300
 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320

<210> 33
<211> 1684
<212> DNA
<213> *Corynebacterium glutamicum*

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                                     Met Asp Glu Ser Arg
                                     1         5

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cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg	163
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala	
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cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt	211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val	
25 30 35	
gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg	259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu	
40 45 50	
gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat	307
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp	
55 60 65	
ggg cct ggt cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat	355
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His	
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Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu	
90 95 100	
gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg	451
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu	
105 110 115	
gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tcg cat	499
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His	
120 125 130	
aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc	547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg	
135 140 145	
cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct	595
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala	
150 155 160 165	
gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct	643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala	
170 175 180	
gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct	691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro	
185 190 195	
gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc	739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg	
200 205 210	
gtg gtg tat acc gct ctg cat ggt gtg ggt ggc cgc gcg atg gcc aat	787
Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn	
215 220 225	
gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag	835
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln	
230 235 240 245	
cag tat cct gat ccc acc ttc ccc act gtg gcg ttc ccc aat ccg gaa	883

Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu	
				250					255					260		
gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cgc	gca	aag	gaa	aag	aac	931
Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn	
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gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cg	tgt	gct	gtg	979
Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val	
		280					285					290				
ggt	att	cg	acc	gct	gat	ggc	ggc	cac	cga	atg	ctc	tct	ggc	gat	gag	1027
Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	Leu	Ser	Gly	Asp	Glu	
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gtg	ggc	aca	ctt	ttg	gct	act	cg	ttg	gtt	ccg	gag	tat	tcc	ggt	gaa	1075
Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu	
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ggc	cca	cg	ccc	gtg	gtt	gcc	acc	acg	gtg	gtg	tct	tcg	cag	ctt	ctg	1123
Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	Ser	Ser	Gln	Leu	Leu	
			330						335					340		
ggt	atc	atc	gcc	gag	gat	aaa	ggg	tgg	gat	tat	tcc	gag	aca	ctg	acg	1171
Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr	Ser	Glu	Thr	Leu	Thr	
			345					350					355			
gga	ttc	aaa	aat	ctg	tcg	agg	gct	gcc	gat	ggt	ctc	gac	gga	ccg	ctt	1219
Gly	Phe	Lys	Asn	Leu	Ser	Arg	Ala	Ala	Asp	Gly	Leu	Asp	Gly	Pro	Leu	
		360					365					370				
gct	ttc	gct	tat	gag	gaa	gct	gtg	ggc	acc	tgc	ccg	gtt	cca	gat	gtc	1267
Ala	Phe	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Thr	Cys	Pro	Val	Pro	Asp	Val	
	375					380				385						
gtg	ccg	gat	aag	gac	ggc	atc	tct	aca	gcg	ttg	ttc	atg	gcg	tcg	tgg	1315
Val	Pro	Asp	Lys	Asp	Gly	Ile	Ser	Thr	Ala	Leu	Phe	Met	Ala	Ser	Trp	
390					395					400					405	
gct	gcc	gaa	ctg	aag	gct	cag	ggc	gca	agc	ctg	cag	caa	aaa	ctc	aat	1363
Ala	Ala	Glu	Leu	Lys	Ala	Gln	Gly	Ala	Ser	Leu	Gln	Gln	Lys	Leu	Asn	
			410					415						420		
gag	ttg	tat	cg	cga	tat	ggg	tat	ttt	gcg	tcc	tcg	caa	att	gct	gtg	1411
Glu	Leu	Tyr	Arg	Arg	Tyr	Gly	Tyr	Phe	Ala	Ser	Ser	Gln	Ile	Ala	Val	
			425					430					435			
cg	acg	agc	agt	cca	cg	gag	tta	gtt	gat	cac	tgg	att	gcg	cat	cct	1459
Arg	Thr	Ser	Ser	Pro	Arg	Glu	Leu	Val	Asp	His	Trp	Ile	Ala	His	Pro	
		440					445					450				
cag	caa	gaa	ctc	att	gga	gtg	tct	gtc	acc	cca	cat	att	ctt	cct	gaa	1507
Gln	Gln	Glu	Leu	Ile	Gly	Val	Ser	Val	Thr	Pro	His	Ile	Leu	Pro	Glu	
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Lys	Gln	Gly	Ile	Ala	Leu	His	Gly	Gln	Val	Gly	His	Val	His	Ile	Arg	
470					475				480						485	
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Ala	Ile	Gly	Arg	Val	Ser	Gly	Thr	Glu	Ala	Lys	Ala	Lys	Leu	Tyr	Leu	

490										495					500					
gaa gtt ggt	cag gcc agc tcc cat	gat gaa gca gct	cag ttg ttg cat	1651																
Glu Val Gly	Gln Ala Ser Ser His	Asp Glu Ala Ala	Gln Leu Leu His																	
505		510	515																	

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Gln Leu Glu	Asp Glu Val Gln	Ser Trp Leu Ser	
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<210> 34

<211> 528

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

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Pro Val Gly	Pro Ala Arg	His Gln Met	Asn Val Leu	Gln Val Thr	Arg
20		25		30	

Thr Thr Ala	Gly Val Ala	Ser Trp Leu	Ala Glu Arg	Ala Ala Leu	Asn
35		40		45	

Pro Val Pro	His Leu Val	Pro Glu Asp	Glu Thr Gly	Ile Gly Arg	Ala
50		55		60	

Leu Tyr Pro	Gln Asp Gly	Pro Leu Arg	Val Val Val	Gly Tyr Asp	Ala
65		70		75	80

Arg Tyr Gly	Ser His Thr	Phe Ala Ala	Thr Thr Ala	Glu Val Phe	Ala
	85		90		95

Gly Ala Gly	Phe Glu Val	Thr Leu Leu	Pro Thr Pro	Ser Pro Thr	Pro
	100		105		110

Leu Ile Pro	Trp Leu Val	Asn Lys His	Gly Leu Asp	Ala Gly Val	Gln
115		120		125	

Ile Thr Ala	Ser His Asn	Gly Ala Ala	Asp Asn Gly	Tyr Lys Val	Phe
130		135		140	

Leu Ser Asn	Gly Arg Gln	Leu Tyr Ser	Glu Leu Glu	Pro Glu Leu	Glu
145		150		155	160

Ala His Ile	Asn Ala Val	Glu Asp Pro	Ile Arg Val	Pro Arg Val	Thr
	165		170		175

Val Arg Pro	Thr Ala Asp	Gln Leu Arg	Arg Tyr Val	Asp Glu Met	Val
	180		185		190

Ser Leu Val	Thr Pro Asp	Gln Ala Asp	Leu Leu Arg	Val Asn Ser	Glu
195		200		205	

Arg Gly Asn	Leu Arg Val	Val Tyr Thr	Ala Leu His	Gly Val Gly	Gly
210		215		220	

Arg Ala Met	Ala Asn Ala	Phe Gln Phe	Ala Gly Phe	Pro His Thr	His
225		230		235	240

Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
 290 295 300
 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320
 Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
 325 330 335
 Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
 340 345 350
 Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
 355 360 365
 Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
 370 375 380
 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
 385 390 395 400
 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
 405 410 415
 Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
 420 425 430
 Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
 435 440 445
 Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
 450 455 460
 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
 465 470 475 480
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
 485 490 495
 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
 500 505 510
 Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
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<210> 35

<211> 536

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(513)

<223> RXA00511

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Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys	
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gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc	144
Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser	
35 40 45	
ctg ggc ggc gag caa tct ggc cac att gtt ctt cca gat cat ggc acc	192
Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr	
50 55 60	
act ggc gat gga act ttg act ggt ctt tcc atc atg gcg cgc atg gct	240
Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala	
65 70 75 80	
gaa acc gga aag tcc ttg ggc gag ttg gca caa gct atg acg gtg ctg	288
Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu	
85 90 95	
cca cag gtt ctg atc aat gtg cca gtt tcc gat aag tcc acc atc gtg	336
Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val	
100 105 110	
agc cac cca agc gtt gtg gct gcg atc gcg gaa gca gaa gct gag ttg	384
Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu	
115 120 125	
ggc gcc acc ggt cgc gtt ctt ctt cgt gct tct ggc acc gaa gag ctt	432
Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu	
130 135 140	
ttc cgc gtg atg gtt gag gct gga gac aag gaa caa gct cgt cgt atc	480
Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile	
145 150 155 160	
gcg gga cgt ctt gct gca gtg gtt gca gaa gtc taattcactt cagtcacagc	533
Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val	
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<210> 36

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 36

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 20 25 30

Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
 35 40 45

Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
 50 55 60

Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65 70 75 80

Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
 85 90 95

Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
 100 105 110

Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125

Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
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Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
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Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
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<210> 37

<211> 1497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1474)

<223> RXN01365

<400> 37

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 Met Arg Thr Arg Glu
 1 5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
 25 30 35

cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259

Arg	Leu	Met	Arg	Ser	Glu	Gly	Glu	Thr	Thr	Val	Ala	Ile	Gly	His	Asp		
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Met	Arg	Asp	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Ala	Phe	Ala	Asp	Gly	Val		
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Thr	Ala	Gln	Gly	Leu	Asp	Val	Val	His	Leu	Gly	Leu	Thr	Ser	Thr	Asp		
		70			75					80					85		
gag	ctg	tac	ttt	gcg	tcc	gga	acc	ttg	aag	tgt	gct	ggt	gcg	atg	ttt	403	
Glu	Leu	Tyr	Phe	Ala	Ser	Gly	Thr	Leu	Lys	Cys	Ala	Gly	Ala	Met	Phe		
				90					95					100			
act	gcg	tcg	cat	aac	ccc	gct	gag	tac	aac	ggc	atc	aag	ttg	tgt	cgt	451	
Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly	Ile	Lys	Leu	Cys	Arg		
			105					110					115				
gcg	ggt	gct	cgt	ccg	gtc	ggt	cag	gat	tct	ggt	ttg	gcc	aac	atc	att	499	
Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile		
		120				125						130					
gat	gat	ctg	ggt	gag	ggt	ggt	cca	gcg	ttt	gat	ggt	gag	tca	ggt	tcg	547	
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser		
		135				140					145						
ggt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595	
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu		
		150			155					160					165		
ctt	ggt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	ggt	gct	gtg	gat	gcg	643	
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala		
				170					175					180			
gca	aac	ggc	atg	ggt	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggt	ctg	691	
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu		
			185					190					195				
cca	ctt	gat	ggt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739	
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro		
		200					205					210					
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	ggt	gat	ttg	cag	787	
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln		
		215				220					225						
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggt	ttg	gcg	ttc	gac	ggc	835	
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly		
		230			235					240					245		
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883	
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser		
				250					255					260			
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931	
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu		
			265					270					275				
ccg	ggt	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979	
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro		

280 285 290
 gag gtg att gct gaa aac ggt ggc act gcg gtg cgt act cgc gtg ggt 1027
 Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val Arg Thr Arg Val Gly
 295 300 305
 cac tcc ttc atc aag gcg aag atg gca gag acc ggt gcg gcc ttt ggt 1075
 His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr Gly Ala Ala Phe Gly
 310 315 320 325
 ggc gag cac tct gcg cac tac tac ttc act gag ttc ttc aat gcg gac 1123
 Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu Phe Phe Asn Ala Asp
 330 335 340
 tcc ggc att ttg gct gcg atg cac gtg ctg gct gcg ctg gga agc cag 1171
 Ser Gly Ile Leu Ala Ala Met His Val Leu Ala Ala Leu Gly Ser Gln
 345 350 355
 gac cag cca ctc agt gag atg atg gct agg tat aac cgg tac gtt gct 1219
 Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr Asn Arg Tyr Val Ala
 360 365 370
 tca ggc gag ttg aac tcc cgt ttg gct aat gca gag gcg cag caa gag 1267
 Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala Glu Ala Gln Gln Glu
 375 380 385
 cgc acc cag gct gtg ctc gat gcg ttc gct gat cgc acc gag tcc gtg 1315
 Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp Arg Thr Glu Ser Val
 390 395 400 405
 gac acc ctt gac ggc gtg act gtg gaa ctc aag gac acc tcc gcg tgg 1363
 Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys Asp Thr Ser Ala Trp
 410 415 420
 ttc aac gtg cgt gcg tcc aac acc gag ccg ctg ctt cgc ctc aat gtt 1411
 Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu Leu Arg Leu Asn Val
 425 430 435
 gaa gct gca tcg aag gaa gaa gtc gat gcg ttg gta gcg gag att cta 1459
 Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu Val Ala Glu Ile Leu
 440 445 450
 ggg att atc cgc gca taatcccatt ttccggcggg cat 1497
 Gly Ile Ile Arg Ala
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<210> 38

<211> 458

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

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Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
 35 40 45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
 260 265 270
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
 275 280 285
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val
 290 295 300
 Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr
 305 310 315 320
 Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu
 325 330 335
 Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala
 340 345 350
 Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr
 355 360 365

Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala
 370 375 380
 Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp
 385 390 395 400
 Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys
 405 410 415
 Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu
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 Val Ala Glu Ile Leu Gly Ile Ile Arg Ala
 450 455

<210> 39
 <211> 994
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> FRXA01365

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 Met Arg Thr Arg Glu
 1 5
 tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20
 gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
 25 30 35
 cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259
 Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
 40 45 50
 atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg 307
 Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
 55 60 65
 act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat 355
 Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
 70 75 80 85
 gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt 403
 Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
 90 95 100
 act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt 451

Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly	Ile	Lys	Leu	Cys	Arg		
			105					110					115				
gcg	ggt	gct	cgt	ccg	gtc	ggg	cag	gat	tct	ggg	ttg	gcc	aac	atc	att	499	
Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile		
			120				125					130					
gat	gat	ctg	gtt	gag	ggg	gtt	cca	gcg	ttt	gat	ggg	gag	tca	ggg	tcg	547	
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser		
			135			140					145						
gtt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595	
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu		
150					155					160					165		
ctt	gtt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	gtt	gct	gtg	gat	gcg	643	
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala		
				170				175						180			
gca	aac	ggc	atg	ggg	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggg	ctg	691	
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu		
			185					190					195				
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739	
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro		
			200				205					210					
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	gtt	gat	ttg	cag	787	
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln		
			215			220					225						
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggg	ttg	gcg	ttc	gac	ggc	835	
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly		
230					235					240					245		
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883	
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser		
				250				255						260			
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931	
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu		
			265					270					275				
ccg	ggg	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979	
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro		
			280				285					290					
gag	gtg	att	gct	gaa												994	
Glu	Val	Ile	Ala	Glu													
			295														

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<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
 20 25 30
 Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
 35 40 45
 Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
 260 265 270
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
 275 280 285
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu
 290 295

<210> 41

<211> 1743

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS
 <222> (101)..(1720)
 <223> RXA00098

<400> 41

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taacctgaag atgttatttta acgacaataa aggagttttc atg gcg gac att tcg 115
 Met Ala Asp Ile Ser
 1 5

acc acc cag gtt tgg caa gac ctg acc gat cat tac tca aac ttc cag 163
 Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn Phe Gln
 10 15 20

gca acc act ctg cgt gaa ctt ttc aag gaa gaa aac cgc gcc gag aag 211
 Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala Glu Lys
 25 30 35

tac acc ttc tcc gcg gct ggc ctc cac gtc gac ctg tcg aag aat ctg 259
 Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys Asn Leu
 40 45 50

ctt gac gac gcc acc ctc acc aag ctc ctt gca ctg acc gaa gaa tct 307
 Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala Leu Thr Glu Glu Ser
 55 60 65

ggc ctt cgc gaa cgc att gac gcg atg ttt gcc ggt gaa cac ctc aac 355
 Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala Gly Glu His Leu Asn
 70 75 80 85

aac acc gaa gac cgc gct gtc ctc cac acc gcg ctg cgc ctt cct gcc 403
 Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala Leu Arg Leu Pro Ala
 90 95 100

gaa gct gat ctg tca gta gat ggc caa gat gtt gct gct gat gtc cac 451
 Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val Ala Ala Asp Val His
 105 110 115

gaa gtt ttg gga cgc atg cgt gac ttc gct act gcg ctg cgc tca ggc 499
 Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr Ala Leu Arg Ser Gly
 120 125 130

aac tgg ttg gga cac acc ggc cac acg atc aag aag atc gtc aac att 547
 Asn Trp Leu Gly His Thr Gly His Thr Ile Lys Lys Ile Val Asn Ile
 135 140 145

ggt atc ggt ggc tct gac ctc gga cca gcc atg gct acg aag gct ctg 595
 Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met Ala Thr Lys Ala Leu
 150 155 160 165

cgt gca tac gcg acc gct ggt atc tca gca gaa ttc gtc tcc aac gtc 643
 Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu Phe Val Ser Asn Val
 170 175 180

gac cca gca gac ctc gtt tct gtg ttg gaa gac ctc gat gca gaa tcc 691
 Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp Leu Asp Ala Glu Ser
 185 190 195

aca ttg ttc gtg atc gct tcg aaa act ttc acc acc cag gag acg ctg 739
 Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Leu

200	205	210	
tcc aac gct cgt gca gct cgt gct tgg ctg gta gag aag ctc ggt gaa			787
Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val Glu Lys Leu Gly Glu			
215	220	225	
gag gct gtc gcg aag cac ttc gtc gca gtg tcc acc aat gct gaa aag			835
Glu Ala Val Ala Lys His Phe Val Ala Val Ser Thr Asn Ala Glu Lys			
230	235	240	245
gtc gca gag ttc ggt atc gac acg gac aac atg ttc ggc ttc tgg gac			883
Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met Phe Gly Phe Trp Asp			
	250	255	260
tgg gtc gga ggt cgt tac tcc gtg gac tcc gca gtt ggt ctt tcc ctc			931
Trp Val Gly Gly Arg Tyr Ser Val Ser Ala Val Gly Leu Ser Leu			
	265	270	275
atg gca gtg atc ggc cct cgc gac ttc atg cgt ttc ctc ggt gga ttc			979
Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg Phe Leu Gly Gly Phe			
	280	285	290
cac gcg atg gat gaa cac ttc cgc acc acc aag ttc gaa gag aac gtt			1027
His Ala Met Asp Glu His Phe Arg Thr Thr Lys Phe Glu Glu Asn Val			
	295	300	305
cca atc ttg atg gct ctg ctc ggt gtc tgg tac tcc gat ttc tat ggt			1075
Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe Tyr Gly			
	310	315	320
gca gaa acc cac gct gtc cta cct tat tcc gag gat ctc agc cgt ttt			1123
Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe			
	330	335	340
gct gct tac ctc cag cag ctg acc atg gaa tca aat ggc aag tca gtc			1171
Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser Asn Gly Lys Ser Val			
	345	350	355
cac cgc gac ggc tcc cct gtt tcc act ggc act ggc gaa att tac tgg			1219
His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp			
	360	365	370
ggt gag cct ggc aca aat ggc cag cac gct ttc ttc cag ctg atc cac			1267
Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu Ile His			
	375	380	385
cag ggc act cgc ctt gtt cca gct gat ttc att ggt ttc gct cgt cca			1315
Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala Arg Pro			
	390	395	400
aag cag gat ctt cct gcc ggt gag cgc acc atg cat gac ctt ttg atg			1363
Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu Leu Met			
	410	415	420
agc aac ttc ttc gca cag acc aag gtt ttg gct ttc ggt aag aac gct			1411
Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys Asn Ala			
	425	430	435
gaa gag atc gct gcg gaa ggt gtc gca cct gag ctg gtc aac cac aag			1459
Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn His Lys			
	440	445	450

gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt 1507
 Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu
 455 460 465

 acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg 1555
 Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val
 470 475 480 485

 atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt 1603
 Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly
 490 495 500

 gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct gtc tct 1651
 Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser
 505 510 515

 ggt gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att 1699
 Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile
 520 525 530

 aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt cag 1743
 Lys Trp Tyr Arg Ala Asn Arg
 535 540

<210> 42
 <211> 540
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 42
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 Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
 35 40 45

 Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
 50 55 60

 Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65 70 75 80

 Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
 85 90 95

 Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
 100 105 110

 Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
 115 120 125

 Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
 130 135 140

 Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
 145 150 155 160

Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
 165 170 175
 Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
 180 185 190
 Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
 195 200 205
 Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
 210 215 220
 Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
 225 230 235 240
 Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
 245 250 255
 Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
 260 265 270
 Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
 275 280 285
 Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
 290 295 300
 Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
 305 310 315 320
 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
 325 330 335
 Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
 340 345 350
 Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
 355 360 365
 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
 370 375 380
 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
 385 390 395 400
 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
 405 410 415
 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
 420 425 430
 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
 435 440 445
 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
 450 455 460
 Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
 465 470 475 480

Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
 485 490 495

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
 500 505 510

Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
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Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
 530 535 540

<210> 43
 <211> 630
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(630)
 <223> RXA01989

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 Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
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 Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
 20 25 30

ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat 144
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45

gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca 192
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60

gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct 240
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80

gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag 288
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95

tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct 336
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110

aaa tct ggt aca act aca gaa cca gca gtt gca ttt aga ttg ttc aaa 384
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125

caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata 432
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140

ttt gca aca acg gat aaa gaa aaa ggt gct tta aaa cag ttg gct aca 480

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga 528
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga 576
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190
 att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa 624
 Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
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 tta tct 630
 Leu Ser
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 20 25 30
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140
 Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190

Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205

Leu Ser
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 Val Lys Leu Val Ile
 1 5

gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc 163
 Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly
 10 15 20

acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc 211
 Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala
 25 30 35

tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga 259
 Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly
 40 45 50

cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg 307
 Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val
 55 60 65

gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg 355
 Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg
 70 75 80 85

tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag 403
 Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys
 90 95 100

gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt 451
 Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg
 105 110 115

gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct 499
 Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala
 120 125 130

gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta 547
 Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val
 135 140 145

tct tct gct tct tcg gtt gcg ggc tca gag aaa gaa gac ctc aac tgc	595
Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys	
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acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act	643
Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr	
170 175 180	
cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc	691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg	
185 190 195	
ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa	739
Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys	
200 205 210	
caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac	787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp	
215 220 225	
gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca	835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala	
230 235 240 245	
gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc	883
Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile	
250 255 260	
gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac	931
Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His	
265 270 275	
gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta	979
Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val	
280 285 290	
gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa	1027
Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys	
295 300 305	
aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg	1075
Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu	
310 315 320 325	
gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg	1123
Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu	
330 335 340	
gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg	1171
Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser	
345 350 355	
ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg	1219
Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu	
360 365 370	
ttc aac gac acc tca cac ctg gaa gcg tgacgacagt ctgacggaag	1266
Phe Asn Asp Thr Ser His Leu Glu Ala	
375 380	
ctc	1269

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 <213> Corynebacterium glutamicum

<400> 46
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 35 40 45
 Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu
 50 55 60
 Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu
 65 70 75 80
 Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu
 85 90 95
 Ala Ile Glu Ala Lys Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr
 100 105 110
 Thr Trp Ile Pro Arg Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn
 115 120 125
 Val Ala Met Asp Ala Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly
 130 135 140
 Asp Ser Ala Ser Val Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys
 145 150 155 160
 Glu Asp Leu Asn Cys Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala
 165 170 175
 Thr Thr Asp Pro Thr Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala
 180 185 190
 Met Ser Val Ala Arg Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser
 195 200 205
 Glu Leu Gly Glu Lys Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln
 210 215 220
 Thr Gly Gly Ile Asp Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met
 225 230 235 240
 Gln Thr Ala Glu Ala Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val
 245 250 255
 Ile Asp Asp Leu Ile Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser
 260 265 270
 Phe Ser Glu Ala His Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu
 275 280 285

Thr Asp Ser Ser Val Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val
 290 295 300

Asn Arg Arg Val Lys Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly
 305 310 315 320

Ala Ala Asn Val Leu Val Val Ser His Val Thr Pro Ile Lys Ala Ile
 325 330 335

Met Arg Gln Ala Leu Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His
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Leu Asp Leu Ala Ser Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro
 355 360 365

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 370 375 380

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXA02492

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 Met Thr Asn Gly Lys
 1 5

ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag 163
 Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
 10 15 20

ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag 211
 Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
 25 30 35

gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc 259
 Ala Lys Gly Val Leu Pro Gly Val Tyr Thr Ser Leu Leu Arg Arg
 40 45 50

gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg 307
 Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
 55 60 65

atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca 355
 Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
 70 75 80 85

ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac 403
 Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
 90 95 100

cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc 451
 Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
 105 110 115
 gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac 499
 Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
 120 125 130
 ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt 547
 Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
 135 140 145
 ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc 595
 Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
 150 155 160 165
 gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt 643
 Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
 170 175 180
 aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc 691
 Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
 185 190 195
 cca acc ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta 739
 Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val
 200 205 210
 gta aac cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc 787
 Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly
 215 220 225
 gca gca gca gta gca aac cag ggt aat aag tagctatttg taggtgagca 837
 Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
 230 235
 ctc 840

<210> 48

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

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 20 25 30

Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr
 35 40 45

Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala
 50 55 60

Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu
 65 70 75 80

Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu

				85					90					95					
Lys	Tyr	Gly	Asp	Asp	Gln	Phe	Met	Glu	Trp	Arg	Arg	Ser	Tyr	Asp	Thr				
			100					105					110						
Pro	Pro	Pro	Glu	Leu	Ala	Asp	Asp	Ala	Glu	Tyr	Ser	Gln	Ala	Asn	Asp				
		115					120					125							
Pro	Arg	Tyr	Ala	Asp	Leu	Asp	Val	Val	Pro	Arg	Thr	Glu	Cys	Leu	Lys				
	130					135					140								
Asp	Val	Val	Val	Arg	Phe	Val	Pro	Tyr	Phe	Glu	Glu	Glu	Ile	Leu	Pro				
145					150					155					160				
Arg	Ala	Lys	Lys	Gly	Glu	Thr	Val	Leu	Ile	Ala	Ala	His	Gly	Asn	Ser				
				165					170					175					
Leu	Arg	Ala	Leu	Val	Lys	His	Leu	Asp	Gly	Ile	Ser	Asp	Ala	Asp	Ile				
			180					185					190						
Ala	Glu	Leu	Asn	Ile	Pro	Thr	Gly	Ile	Pro	Leu	Val	Tyr	Glu	Ile	Ala				
		195					200					205							
Glu	Asp	Gly	Ser	Val	Val	Asn	Pro	Gly	Gly	Thr	Tyr	Leu	Asp	Pro	Glu				
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Ala	Ala	Ala	Ala	Gly	Ala	Ala	Ala	Val	Ala	Asn	Gln	Gly	Asn	Lys					
225					230					235									

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<211> 729
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA00381
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				Met	Thr	Gln	Thr	Ile							
				1				5							
gtc cat cta gtt	cg	cac	ggc	gaa	gtc	cac	aac	cca	gag	aaa	atc	ctg	163		
Val His Leu Val	Arg	His	Gly	Glu	Val	His	Asn	Pro	Glu	Lys	Ile	Leu			
	10					15					20				
tac gga cgc atg	ccc	gga	tac	agg	ttg	tct	tcc	cgt	gga	cgc	agc	caa	211		
Tyr Gly Arg Met	Pro	Gly	Tyr	Arg	Leu	Ser	Ser	Arg	Gly	Arg	Ser	Gln			
	25				30					35					
gcc gcc cgc act	gca	gct	tct	ttt	gaa	ggc	cac	gat	gtc	acc	tac	att	259		
Ala Ala Arg Thr	Ala	Ala	Ser	Phe	Glu	Gly	His	Asp	Val	Thr	Tyr	Ile			
	40			45					50						
gcg gcc tcc cca	ttg	cag	cgt	gtg	cag	gaa	acc	tcc	gaa	ccg	ttc	atc	307		
Ala Ala Ser Pro	Leu	Gln	Arg	Val	Gln	Glu	Thr	Ser	Glu	Pro	Phe	Ile			

55	60	65	
aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca			355
Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala			
70	75	80	85
ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg			403
Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu			
90	95		100
tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc			451
Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser			
105	110		115
tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg			499
Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val			
120	125		130
gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc			547
Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr			
135	140		145
cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc			595
His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser			
150	155		160
ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca			643
Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr			
170	175		180
tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa			691
Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu			
185	190		195
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Pro Ala Gln Glu Ile			
200			

<210> 50

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn

1

5

10

15

Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser

20

25

30

Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His

35

40

45

Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr

50

55

60

Ser Glu Pro Phe Ile Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu

65

70

75

80

Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly

	85		90		95
Trp Arg Ser Gln Leu Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn	100		105		110
Pro Thr Leu Pro Ser Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg	115		120		125
Met Met Ala Ala Val Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu	130		135		140
Ala Ile Leu Val Thr His Gln Leu Pro Ile Val Cys Val Gln Arg His	145		150		155
					160
Ala Arg Gly Gln Ser Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp	165		170		175
Leu Ala Ser Val Thr Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly	180		185		190
Val His Tyr Asn Glu Pro Ala Gln Glu Ile	195		200		

<210> 51

<211> 822

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(799)

<223> RXA02122

<400> 51

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ccttttttta agtgggcggt caggaatttt tcgcacaggt	atg ctg cat gtc atg	115
	Met Leu His Val Met	
	1 5	

aag ccg ggt tca cac gca gct gcc gaa aag act caa tcc act gtg gtt	163
Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr Gln Ser Thr Val Val	
10 15 20	

tta ctc att cgg cat ggg caa acc cca aca act ggt cag gtt ctg cct	211
Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr Gly Gln Val Leu Pro	
25 30 35	

ggt cag acg ccg ggt tta cac ctg tct gat aag ggt gaa gag cag gcg	259
Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys Gly Glu Glu Gln Ala	
40 45 50	

cgg gag gtg gca cag cgt ctg gcg gag gtg ccg att acc gct gtg tat	307
Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro Ile Thr Ala Val Tyr	
55 60 65	

tca tcg ccg atg gag cgt gcg cag gaa aca gca gca ccg acg gtc agc	355
Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala Ala Pro Thr Val Ser	
70 75 80 85	

gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat 403
 Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp
 90 95 100

ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag 451
 Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu
 105 110 115

gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt 499
 Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly
 120 125 130

ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc 547
 Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly
 135 140 145

aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat 595
 Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His
 150 155 160 165

gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg 643
 Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu
 170 175 180

gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg 691
 Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val
 185 190 195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca 739
 Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr
 200 205 210

aat tcc aga aca gga tcg ttg gga tac ctt cga gac aaa ctt ccg aaa 787
 Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys
 215 220 225

gct ccg caa cca tgatcacctc accatttgag cgc 822
 Ala Pro Gln Pro
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<210> 52

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

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Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr
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Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys
 35 40 45

Gly Glu Glu Gln Ala Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro
 50 55 60

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala
 65 70 75 80

Ala	Pro	Thr	Val	Ser 85	Ala	His	Gly	Leu	Glu 90	Leu	Thr	Val	Glu	Pro 95	Gly
Leu	Ile	Glu	Cys 100	Asp	Phe	Gly	Glu	Trp 105	Thr	Gly	Arg	Lys	Leu 110	Thr	Glu
Leu	Asn	Ala 115	Leu	Glu	Glu	Trp	Lys 120	Ala	Val	Gln	Lys	Thr 125	Pro	Ser	Thr
Phe	Arg 130	Phe	Pro	Gly	Gly	Glu	Ser 135	Phe	Val	Glu	Met 140	Gln	Asp	Arg	Met
Val 145	Glu	Ala	Ile	Gly	Asn 150	Ile	Ala	Gln	Gln	His 155	Pro	Gly	Glu	Ile	Val 160
Ala	Ala	Phe	Ser 165	His	Ala	Asp	Thr	Ile	Lys 170	Ala	Ala	Val	Ala	His 175	Phe
Val	Gly	Thr 180	Pro	Leu	Asp	Ser	Phe	Gln 185	Arg	Ile	Phe	Ile	Asp 190	Thr	Ala
Ser	Ile	Ser 195	Ala	Val	Glu	Phe	Thr 200	Gly	Lys	Ser	Ser	Gly 205	Val	Ser	Ser
His 210	Met	Leu	Leu	Thr	Asn 215	Ser	Arg	Thr	Gly	Ser	Leu 220	Gly	Tyr	Leu	Arg
Asp 225	Lys	Leu	Pro	Lys	Ala 230	Pro	Gln	Pro							

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<223> RXA00206
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                                         Met Glu Asp Met Arg
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Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val
                        10                               15                        20

atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc 211
Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val
                        25                               30                        35

gtt ggt tat caa gac ggt tgg gaa gga ctg tta ggc gat cgt cgc gta 259
Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val
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Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly	
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Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly	
70 75 80 85	
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Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu	
90 95 100	
atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct	451
Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser	
105 110 115	
gat aac ggt atc cct gtt gtc ggt gtc cca aag acc att gac aat gac	499
Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp	
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Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val	
135 140 145	
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Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn	
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Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala	
170 175 180	
ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa	691
Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu	
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Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe	
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Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu	
215 220 225	
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Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe	
230 235 240 245	
ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc	883
Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile	
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cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att	931
His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile	
265 270 275	
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Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg	
280 285 290	
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Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
 295 300 305

gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa 1075
 Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu
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gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc 1123
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<213> Corynebacterium glutamicum

<400> 54

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 35 40 45

Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
 50 55 60

Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65 70 75 80

Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
 85 90 95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
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Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
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Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
 165 170 175

Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
 180 185 190

Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala
 195 200 205

Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
 210 215 220

Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly
 225 230 235 240

His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
 245 250 255

Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr
 260 265 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
 275 280 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
 290 295 300

Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met
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Arg Trp Val Thr Ala Gln Ala Met Phe Gly
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<211> 1083

<212> DNA

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<223> RXA01243

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 Met Ile Leu Thr Val
 1 5

act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163
 Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile
 10 15 20

gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211
 Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly
 25 30 35

ggt ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259
 Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu
 40 45 50

act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg 307
 Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu
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Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile Pro Val Ala Gly Pro	
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Ile Pro Met His Leu Thr Met Arg Asp Ala Glu Gly Asn Glu Thr Lys	
90 95 100	
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Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser Gln Leu Ala Ile Leu	
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Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala Ala Trp Val Leu Leu	
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Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala Trp Phe Val Asp Val	
135 140 145	
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Val Arg Ser Leu Arg Leu Tyr His Pro His Val Lys Val Ala Ile Ala	
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gca act ggt gct gcg ttg cgt gcg gtt att cga cag ctt gca gct acg	643
Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg Gln Leu Ala Ala Thr	
170 175 180	
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Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu Ile Glu Ile Ala Thr	
185 190 195	
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Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp Val Glu Gly Asp Leu	
200 205 210	
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Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile Asp Ser Gly Val Thr	
215 220 225	
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Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser Leu Tyr Val Ser Glu	
230 235 240 245	
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Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr Pro Gly Lys Gln Gly	
250 255 260	
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Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe Leu Ala Ala Ser Asn	
265 270 275	
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Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn Ala Val Ala Tyr Ala	
280 285 290	
aac gct gaa ggc agt gag tgg gac aac tac att ccc aca ccc gat aag	1027
Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys	
295 300 305	
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1083

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 <213> Corynebacterium glutamicum

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 35 40 45

Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser
 50 55 60

His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile
 65 70 75 80

Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu
 85 90 95

Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser
 100 105 110

Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala
 115 120 125

Ala Trp Val Leu Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala
 130 135 140

Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val
 145 150 155 160

Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
 165 170 175

Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu
 180 185 190

Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp
 195 200 205

Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile
 210 215 220

Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser
 225 230 235 240

Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr
 245 250 255

Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe

260	265	270
Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn		
275	280	285
Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile		
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Pro Thr Pro Asp Lys Leu Arg Ala Glu His Val Val Ile Lys Ser Leu		
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		320

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 <223> RXA01882

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 Met Ile Ile Thr Phe
 1 5
 acc cca aac ccg agt att gat tcc acg ctg tcg ctc ggc gaa gag ctc 163
 Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
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 tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt 211
 Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
 25 30 35
 ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa 259
 Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
 40 45 50
 acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg 307
 Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
 55 60 65
 gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac 355
 Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
 70 75 80 85
 gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag 403
 Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
 90 95 100
 ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg 451
 Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu
 105 110 115
 gaa aag gtg ctt atc gac gcg ctc cgc ccc gaa gtc acc tgg gtt gtc 499

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Leu	Ala	Gly	Ser	Leu	Pro	Pro	Gly	Ala	Pro	Val	Asp	Trp	Tyr	Ala	Arg		
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ctc	acc	gcg	ttg	atc	cat	tca	gca	cgc	cct	gac	gtt	cgc	gtg	gct	gtc	595	
Leu	Thr	Ala	Leu	Ile	His	Ser	Ala	Arg	Pro	Asp	Val	Arg	Val	Ala	Val		
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gat	acc	tca	gac	aag	cca	ctg	atg	gcg	ttg	ggc	gag	agc	ttg	gat	aca	643	
Asp	Thr	Ser	Asp	Lys	Pro	Leu	Met	Ala	Leu	Gly	Glu	Ser	Leu	Asp	Thr		
				170					175						180		
cct	ggc	gct	gct	ccg	aac	ctg	att	aag	cca	aat	ggc	ctg	gaa	ctg	ggc	691	
Pro	Gly	Ala	Ala	Pro	Asn	Leu	Ile	Lys	Pro	Asn	Gly	Leu	Glu	Leu	Gly		
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Gln	Leu	Ala	Asn	Thr	Asp	Gly	Glu	Glu	Leu	Glu	Ala	Arg	Ala	Ala	Gln		
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Gly	Asp	Tyr	Asp	Ala	Ile	Ile	Ala	Ala	Ala	Asp	Val	Leu	Val	Asn	Arg		
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Val	Asn	Ala	Glu	Gly	Ala	Trp	Thr	Ala	Thr	Ser	Pro	Lys	Ile	Asp	Val		
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gta	tcc	acc	gtt	gga	gct	gga	gac	tgt	gct	ctt	gca	ggc	ttt	gtt	atg	931	
Val	Ser	Thr	Val	Gly	Ala	Gly	Asp	Cys	Ala	Leu	Ala	Gly	Phe	Val	Met		
			265					270					275				
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Ala	Arg	Ser	Gln	Lys	Lys	Thr	Leu	Glu	Glu	Ser	Leu	Leu	Asn	Ala	Val		
		280					285					290					
tct	tac	ggc	tcg	act	gcg	gcg	tct	ctt	cct	ggc	act	acc	att	cct	cgt	1027	
Ser	Tyr	Gly	Ser	Thr	Ala	Ala	Ser	Leu	Pro	Gly	Thr	Thr	Ile	Pro	Arg		
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Pro	Asp	Gln	Leu	Ala	Thr	Ala	Gly	Ala	Thr	Val	Thr	Gln	Val	Lys	Gly		
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<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
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Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
      65           70           75           80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
      85           90           95

Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
      100           105           110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
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Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
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Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
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Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
      165           170           175

Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
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Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
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Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
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Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
      225           230           235           240

Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
      245           250           255

Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
      260           265           270

Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser
      275           280           285

Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
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<223> RXA01702

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Met Pro Ile Ala Thr
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ccc gag gtc tat aac gag atg ctc gat cgt gct aag gaa ggc gga ttc 163
Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Gly Phe
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gcc ttc cca gcc atc aac tgc acc tcc tgc gaa acc atc aac gca gct 211
Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala
25 30 35

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Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser
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acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc 307
Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val
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aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc 355
Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser
70 75 80 85

tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc 403
Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val
90 95 100

ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc 451
Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val
105 110 115

gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc 499
Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser
120 125 130

gct gtc cca atc gac gag aac ctc gaa atc gca cag gag ctg ctg gct 547
Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala
135 140 145

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Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val
150 155 160 165

ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac 643
 Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr
 170 175 180

acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt 691
 Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly
 185 190 195

gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc 739
 Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly
 200 205 210

gtt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag 787
 Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu
 215 220 225

ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt 835
 Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu
 230 235 240 245

cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag 883
 Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys
 250 255 260

atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act 931
 Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr
 265 270 275

gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag 979
 Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu
 280 285 290

aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag 1027
 Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys
 295 300 305

gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct 1075
 Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser
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gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc 1123
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 35 40 45
 Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala
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 Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His
 65 70 75 80
 Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His
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 Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile
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 Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His
 115 120 125
 Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
 130 135 140
 Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val
 145 150 155 160
 Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
 165 170 175
 Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp
 180 185 190
 Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe
 195 200 205
 Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
 210 215 220
 Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu
 225 230 235 240
 Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
 245 250 255
 Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys
 260 265 270
 Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
 275 280 285
 Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu
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 Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala
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Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val Thr Phe Gly Ala Gln
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Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr Gly Glu Val Ser Ala
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Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val Val Val Gly His Ser
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Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu Leu Val Ala Ala Lys
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Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro Ile Val Cys Val Gly
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Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His Val Glu Tyr Val Val
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Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp Ala Ala Glu Leu Ala
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Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys
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 Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile
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ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt 787
 Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly
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cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt 835
 Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly
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gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct 877
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Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
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Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val
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Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
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Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
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Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
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Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
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Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
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Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp
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Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
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Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
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Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala
 195 200 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val
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 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
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 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
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Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly	
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Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala	
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Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile	
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Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln	
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Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr	
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Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
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 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
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 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
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 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
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 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
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Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
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 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
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 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
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 Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
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 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190
 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
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 Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220
 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
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 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
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 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
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 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
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 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
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 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
 405 410 415

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
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Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
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 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
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 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
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 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
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 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
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 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
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 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

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 Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
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Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile	
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Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp	
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Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp	
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Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly	
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Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala	
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Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile	
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Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr	
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Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys	
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Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys	
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Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln	
265 270 275	
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Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu	
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Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr	
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Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys	
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Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly	
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Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
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 375 380 385
 aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
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 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
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 35 40 45
 Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60
 Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
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 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
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 Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125
 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140
 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160
 Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175
 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190
 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205
 Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220
 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
 225 230 235 240
 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
 260 265 270
 Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
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 Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
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 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
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 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
 325 330 335
 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
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 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
 355 360 365
 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
 370 375 380
 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
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 Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
 420 425 430
 Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn

435					440					445					
Glu	Phe	Gly	Tyr	Ser	Asn	Gln	Val	Ile	Arg	Ile	Val	Glu	Glu	Ile	Ala
	450					455					460				
Gly	Val	Arg	Pro	Arg	Val	Tyr	Pro	Glu	Arg	Arg	Gln	Pro	Ala	Val	Leu
465					470					475					480

<210> 67
<211> 1125
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>
<221> CDS
<222> (101)..(1102)
<223> RXA02256
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<400> 67																
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gacacattgc atttctaca atcttttagag gagacacaac						atg	acc	att	cgt	gtt	115					
						Met	Thr	Ile	Arg	Val						
						1							5			
ggt att aac gga ttt ggc cgt atc gga cgt aac ttc ttc cgc gca gtt	163															
Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn Phe Phe Arg Ala Val																
						10							20			
						15										
ctg gag cgc agc gac gat ctc gag gta gtt gca gtc aac gac ctc acc	211															
Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala Val Asn Asp Leu Thr																
						25							35			
						30										
gac aac aag acc ctt tcc acc ctt ctc aag ttc gac tcc atc atg ggc	259															
Asp Asn Lys Thr Leu Ser Thr Leu Lys Phe Asp Ser Ile Met Gly																
						40							50			
						45										
cgc ctt ggc cag gaa gtt gaa tac gac gat gac tcc atc acc gtt ggt	307															
Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp Ser Ile Thr Val Gly																
						55							65			
						60										
ggc aag cgc atc gct gtt tac gca gag cgc gat cca aag aac ctg gac	355															
Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp Pro Lys Asn Leu Asp																
						70							85			
						75										
tggt gct gca cac aac gtt gac atc gtg atc gag tcc acc ggc ttc ttc	403															
Trp Ala Ala His Asn Val Asp Ile Val Ile Glu Ser Thr Gly Phe Phe																
						90							100			
						95										
acc gat gca aac gcg gct aag gct cac atc gaa gca ggt gcc aag aag	451															
Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu Ala Gly Ala Lys Lys																
						105							115			
						110										
gtc atc atc tcc gca cca gca agc aac gaa gac gca acc ttc gtt tac	499															
Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp Ala Thr Phe Val Tyr																
						120							130			
						125										

ggt gtg aac cac gag tcc tac gat cct gag aac cac aac gtg atc tcc 547
 Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn His Asn Val Ile Ser
 135 140 145

ggc gca tct tgc acc acc aac tgc ctc gca cca atg gca aag gtc cta 595
 Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Val Leu
 150 155 160 165

aac gac aag ttc ggc atc gag aac ggc ctc atg acc acc gtt cac gca 643
 Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met Thr Thr Val His Ala
 170 175 180

tac act ggc gac cag cgc ctg cac gat gca cct cac cgc gac ctg cgt 691
 Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro His Arg Asp Leu Arg
 185 190 195

cgt gca cgt gca gca gca gtc aac atc gtt cct acc tcc acc ggt gca 739
 Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro Thr Ser Thr Gly Ala
 200 205 210

gct aag gct gtt gct ctg gtt ctc cca gag ctc aag ggc aag ctt gac 787
 Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys Leu Asp
 215 220 225

ggc tac gca ctt cgc gtt cca gtt atc acc ggt tcc gca acc gac ctg 835
 Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly Ser Ala Thr Asp Leu
 230 235 240 245

acc ttc aac acc aag tct gag gtc acc gtt gag tcc atc aac gct gca 883
 Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu Ser Ile Asn Ala Ala
 250 255 260

atc aag gaa gct gca gtc ggc gag ttc ggc gag acc ctg gct tac tcc 931
 Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu Thr Leu Ala Tyr Ser
 265 270 275

gaa gag cca ctg gtt tcc acc gac atc gtc cac gat tcc cac ggc tcc 979
 Glu Glu Pro Leu Val Ser Thr Asp Ile Val His Asp Ser His Gly Ser
 280 285 290

atc ttc gac gct ggc ctg acc aag gtc tcc ggc aac acc gtc aag gtt 1027
 Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly Asn Thr Val Lys Val
 295 300 305

gtt tcc tgg tac gac aac gag tgg ggc tac acc tgc cag ctc ctg cgt 1075
 Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr Cys Gln Leu Leu Arg
 310 315 320 325

ctg acc gag ctc gta gct tcc aag ctc taattagttc acatcgctaa 1122
 Leu Thr Glu Leu Val Ala Ser Lys Leu
 330

cgt 1125

<210> 68

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Met Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
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 Phe Phe Arg Ala Val Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala
 20 25 30
 Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe
 35 40 45
 Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp
 50 55 60
 Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp
 65 70 75 80
 Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
 85 90 95
 Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu
 100 105 110
 Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
 115 120 125
 Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn
 130 135 140
 His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
 145 150 155 160
 Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met
 165 170 175
 Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
 180 185 190
 His Arg Asp Leu Arg Arg Ala Arg Ala Ala Val Asn Ile Val Pro
 195 200 205
 Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
 210 215 220
 Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly
 225 230 235 240
 Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu
 245 250 255
 Ser Ile Asn Ala Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu
 260 265 270
 Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His
 275 280 285
 Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly
 290 295 300
 Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
 305 310 315 320
 Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu

325

330

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<210> 69
<211> 1338
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1315)  
<223> RXA02257
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<400> 69																
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gaagaatttt ttaaacaatc aaatctccaa ggagtacggc atg gct gtt aag acc 115																
Met Ala Val Lys Thr 5																
ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt 163																
Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val 20																
cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat 211																
Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp 35																
aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa 259																
Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu 50																
ggg ggc gca aag gtc atc gtc atg gct cac ctt ggc cgc cca aag ggc 307																
Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly 65																
gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc 355																
Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser 85																
gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa 403																
Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu 100																
gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc 451																
Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu 115																
ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca 499																
Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala 130																
gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac 547																
Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn 145																
ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc 595																
Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr 165																
tcc gtc tac gac att gca aag ttg ctg cca cac tac gct ggc gga ctg 643																

Ser Val Tyr Asp	Ile Ala Lys Leu Leu	Pro His Tyr Ala Gly Gly Leu	
	170	175	180
gta gag acc gag att tcc gtt ctg gaa aag atc gca gaa tca cca gag			691
Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile Ala Glu Ser Pro Glu			
	185	190	195
gca cca tac gta gtg gtt ctc ggt gga tcc aag gtc tct gac aag atc			739
Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys Val Ser Asp Lys Ile			
	200	205	210
ggt gtt att gag gcg ctg gct gcc aag gct gac aag atc atc gtc ggt			787
Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp Lys Ile Ile Val Gly			
	215	220	225
ggc ggc atg tgc tac acc ttc ctc gca gct cag gga cac aac gtt cag			835
Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln Gly His Asn Val Gln			
	230	235	240
cag tcc ctc ctg cag gaa gaa atg aag gct acc tgc acc gac ctg ctc			883
Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr Cys Thr Asp Leu Leu			
	250	255	260
gca cgc ttc ggt gac aag atc gtt ctc cca gtt gac ctg gtt gca gca			931
Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val Asp Leu Val Ala Ala			
	265	270	275
tcc gaa ttt aac aag gac gca gag aag cag atc gtt gac ctg gac tcc			979
Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile Val Asp Leu Asp Ser			
	280	285	290
atc cca gaa ggc tgg atg tct ctt gac atc gga cca gag tcc gtc aag			1027
Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly Pro Glu Ser Val Lys			
	295	300	305
aac ttc ggt gag gtt ctc agc acc gct aag acc atc ttc tgg aac ggc			1075
Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr Ile Phe Trp Asn Gly			
	310	315	320
cca atg ggc gtg ttc gag ttc gca gca ttc tct gaa ggc acc cgc ggc			1123
Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser Glu Gly Thr Arg Gly			
	330	335	340
atc gcc cag gcc atc atc gat gca act gca ggc aac gac gca ttc tcc			1171
Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly Asn Asp Ala Phe Ser			
	345	350	355
gtt gtt ggc ggt ggc gac tcc gca gca tcc gtt cgc gtg ctc ggc ctg			1219
Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val Arg Val Leu Gly Leu			
	360	365	370
aac gaa gac ggc ttc tcc cac atc tcc acc ggt ggt ggc gca tcc ctc			1267
Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly Gly Gly Ala Ser Leu			
	375	380	385
gag tac ctt gaa ggc aag gaa ctc cca ggc gtt gca att ctc gct cag			1315
Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val Ala Ile Leu Ala Gln			
	390	395	400
taaataccgac acggcccttt gtt			1338

<210> 70

<211> 405

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

Met Ala Val Lys Thr Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly
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Arg His Val Ile Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp
 20 25 30

Arg Glu Ile Thr Asp Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu
 35 40 45

Lys Ala Leu Ser Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
 50 55 60

Gly Arg Pro Lys Gly Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val
 65 70 75 80

Ala Glu Ala Leu Ser Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala
 85 90 95

Asp Val Val Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu
 100 105 110

Gly Asp Ile Leu Leu Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr
 115 120 125

Ser Lys Asp Glu Ala Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala
 130 135 140

Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
 145 150 155 160

His Arg Ala Gln Thr Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His
 165 170 175

Tyr Ala Gly Gly Leu Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile
 180 185 190

Ala Glu Ser Pro Glu Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys
 195 200 205

Val Ser Asp Lys Ile Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp
 210 215 220

Lys Ile Ile Val Gly Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln
 225 230 235 240

Gly His Asn Val Gln Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr
 245 250 255

Cys Thr Asp Leu Leu Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val
 260 265 270

Asp Leu Val Ala Ala Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile
 275 280 285

Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly
 290 295 300

Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr
 305 310 315 320

Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser
 325 330 335

Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly
 340 345 350

Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
 355 360 365

Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly
 370 375 380

Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val
 385 390 395 400

Ala Ile Leu Ala Gln
 405

<210> 71
 <211> 1398
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1375)
 <223> RXA00235

<400> 71
 cgaaacaaga ttogtgcaac aattgggtgt agacgtgatt gaagacattt gatcacgtga 60
 ataattctag ttagctccca agttggcata ggaggccaca gtg gct gaa atc atg 115
 Val Ala Glu Ile Met
 1 5

cac gta ttc gct cgc gaa att ctc gac tcc cgc ggt aac cca acc gtc 163
 His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg Gly Asn Pro Thr Val
 10 15 20

gag gca gag gtt ttc ctg gat gac ggt tcc cac ggt gtc gca ggt gtt 211
 Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His Gly Val Ala Gly Val
 25 30 35

cca tcc ggc gca tcc acc ggc gtc cac gag gct cat gag ctg cgt gac 259
 Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala His Glu Leu Arg Asp
 40 45 50

ggt ggc gat cgc tac ctg ggc aag ggc gtt ttg aag gca gtt gaa aac 307
 Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu Lys Ala Val Glu Asn
 55 60 65

gtc aac gaa gaa atc ggc gac gag ctc gct ggc cta gag gct gac gat 355
 Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly Leu Glu Ala Asp Asp
 70 75 80 85

cag cgc ctc atc gac gaa gca atg atc aag ctt gat ggc acc gcc aac	403
Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu Asp Gly Thr Ala Asn	
90 95 100	
aag tcc cgc ctg ggt gca aac gca atc ctt ggt gtt tcc atg gct gtt	451
Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly Val Ser Met Ala Val	
105 110 115	
gca aag gct gct gct gat tcc gca ggc ctc cca ctg ttc cgc tac atc	499
Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro Leu Phe Arg Tyr Ile	
120 125 130	
ggt gga cca aac gca cac gtt ctt cca gtt cca atg atg aac atc atc	547
Gly Gly Pro Asn Ala His Val Leu Pro Val Pro Met Met Asn Ile Ile	
135 140 145	
acc ggt ggc gct cac gct gac tcc ggt gtt gac gtt cag gaa ttc atg	595
Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp Val Gln Glu Phe Met	
150 155 160 165	
atc gct cca atc ggt gca gag acc ttc tct gag gct ctc cgc aac ggc	643
Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu Ala Leu Arg Asn Gly	
170 175 180	
gcg gag gtc tac cac gca ctg aag tcc gtc atc aag gaa aag ggc ctg	691
Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu	
185 190 195	
tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc	739
Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala Pro Ser Val Gly Ser	
200 205 210	
acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc	787
Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly	
215 220 225	
ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct	835
Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser	
230 235 240 245	
gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc	883
Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser	
250 255 260	
gca gct gag atg gca aac gtt tac gct gag ctc gtt gac gcg tac cca	931
Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro	
265 270 275	
atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac	979
Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr	
280 285 290	
acc aac ctc acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac	1027
Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp	
295 300 305	
gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag	1075
Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys	
310 315 320 325	

aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctc 1123
Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu
330 335 340

acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc 1171
Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr
345 350 355

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tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct    1219
Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala
          360                      365                      370
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gac ctc gca gtt gca ctc aac tgt ggc cag atc aag act ggt gct cca 1267
Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro
375 380 385

gca	cgt	tcc	gac	cgt	gtc	gca	aag	tac	aac	cag	ctt	ctc	cgc	atc	gag	1315
Ala	Arg	Ser	Asp	Arg	Val	Ala	Lys	Tyr	Asn	Gln	Leu	Leu	Arg	Ile	Glu	
390					395					400					405	

cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca 1363
Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro
410 415 420

cgc ttt cag ggc taaataaaaag cgctttttcga cgc 1398
Arg Phe Gln Gly
425

<210> 72

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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Val Ala Glu Ile Met His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg
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Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His
20 25 30

Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
35 40 45

His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
50 55 60

Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly
65 70 75 80

Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu
85 90 95

Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
100 105 110 .

Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro
115 120 125

Leu Phe Arg Tyr Ile Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
130 135 140

Met Met Asn Ile Ile Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp
 145 150 155 160
 Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
 165 170 175
 Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile
 180 185 190
 Lys Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
 195 200 205
 Pro Ser Val Gly Ser Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala
 210 215 220
 Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu
 225 230 235 240
 Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu
 245 250 255
 Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu
 260 265 270
 Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
 275 280 285
 Asp Trp Glu Gly Tyr Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val
 290 295 300
 Gln Ile Val Gly Asp Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys
 305 310 315 320
 Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
 325 330 335
 Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Asp Met Ala His
 340 345 350
 Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
 355 360 365
 Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
 370 375 380
 Lys Thr Gly Ala Pro Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln
 385 390 395 400
 Leu Leu Arg Ile Glu Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly
 405 410 415
 Arg Ser Ala Phe Pro Arg Phe Gln Gly
 420 425

<210> 73

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXA01093

<400> 73

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gtagtacctg tggcttgagg gggaatgacg tactaggctt atg ggc gtg gat aga 115
                                         Met Gly Val Asp Arg
                                         1 5

cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat 163
Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp
          10          15          20

gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac 211
Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn
          25          30          35

ttc tcc cat ggt gac cac cca gat cat gag caa aac tac aag tgg gtc 259
Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
          40          45          50

cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac 307
Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp
          55          60          65

ctc caa gga ccg aag atc cgt ctt ggc cgt ttc act gac ggc gca acc 355
Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr
          70          75          80          85

gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag 403
Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu
          90          95          100

gga acg cac gat cgt gtg tcc acc acc tac aag aat ctg gca aaa gac 451
Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp
          105          110          115

gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc 499
Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu
          120          125          130

gtc tgc gtt tcc gtc gaa ggt aac gac gtc atc tgt gag gtt gtt gag 547
Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu
          135          140          145

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Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp
          150          155          160          165

att tcc gta cct gca ctg tcc gaa aag gat atc cgt gac ctg cgc ttc 643
Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe
          170          175          180

gcc ctg aag ctc ggc gtg gac ttt att gca ctg tcc ttc gta cgt tcc 691
Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser
          185          190          195

cca gca gat gct gaa ctc gtt cac aag atc atg gac gaa gaa ggt cgt 739

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Pro	Ala	Asp	Ala	Glu	Leu	Val	His	Lys	Ile	Met	Asp	Glu	Glu	Gly	Arg		
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Arg	Val	Pro	Val	Ile	Ala	Lys	Leu	Glu	Lys	Pro	Glu	Ala	Val	Thr	Ser		
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Leu	Glu	Pro	Ile	Val	Leu	Ala	Phe	Asp	Ala	Val	Met	Val	Ala	Arg	Gly		
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gac	ctc	ggc	gtt	gag	gtt	cct	ctg	gag	gag	gtt	cca	ctg	gtt	cag	aag	883	
Asp	Leu	Gly	Val	Glu	Val	Pro	Leu	Glu	Glu	Val	Pro	Leu	Val	Gln	Lys		
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Arg	Ala	Ile	Gln	Ile	Ala	Arg	Glu	Asn	Ala	Lys	Pro	Val	Ile	Val	Ala		
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Thr	Gln	Met	Leu	Asp	Ser	Met	Ile	Glu	Asn	Ser	Arg	Pro	Thr	Arg	Ala		
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Met	Leu	Ser	Gly	Glu	Thr	Ser	Val	Gly	Lys	Asp	Pro	His	Asn	Val	Val		
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Arg	Thr	Met	Ser	Arg	Ile	Val	Arg	Phe	Ala	Glu	Thr	Asp	Gly	Arg	Val		
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Pro	Asp	Leu	Thr	His	Ile	Pro	Arg	Thr	Lys	Arg	Gly	Val	Ile	Ser	Tyr		
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Ser	Ala	Arg	Asp	Ile	Ala	Glu	Arg	Leu	Asn	Ala	Arg	Ala	Leu	Val	Ala		
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ttc	acc	acc	tct	ggc	gat	acc	gca	aag	cgt	gtg	gct	cgt	ctg	cac	agc	1267	
Phe	Thr	Thr	Ser	Gly	Asp	Thr	Ala	Lys	Arg	Val	Ala	Arg	Leu	His	Ser		
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cac	ctg	cca	ctg	ctc	gtg	ttc	act	cca	aat	gag	gca	gtt	cgc	tct	gag	1315	
His	Leu	Pro	Leu	Leu	Val	Phe	Thr	Pro	Asn	Glu	Ala	Val	Arg	Ser	Glu		
390					395					400					405		
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Leu	Ala	Leu	Thr	Trp	Gly	Ala	Thr	Thr	Phe	Leu	Cys	Pro	Pro	Val	Ser		
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gat	acc	gat	gac	atg	atg	cgc	gaa	gtc	gac	cgt	gct	ctt	tta	gca	atg	1411	
Asp	Thr	Asp	Asp	Met	Met	Arg	Glu	Val	Asp	Arg	Ala	Leu	Leu	Ala	Met		
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Pro	Glu	Tyr	Asn	Lys	Gly	Asp	Met	Met	Val	Val	Val	Ala	Gly	Ser	Pro		

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 Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly
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 gac gac aca agg att gca aag ctc taatcgctta aatctttcaa aaa 1554
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 Asn Tyr Lys Trp Val Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val
 50 55 60
 Gly Ile Leu Ala Asp Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe
 65 70 75 80
 Thr Asp Gly Ala Thr Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr
 85 90 95
 Val Asp Asp Val Glu Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys
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 Asn Leu Ala Lys Asp Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp
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 Gly Lys Val Gly Leu Val Cys Val Ser Val Glu Gly Asn Asp Val Ile
 130 135 140
 Cys Glu Val Val Glu Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser
 145 150 155 160
 Leu Pro Gly Met Asp Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile
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 Arg Asp Leu Arg Phe Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu
 180 185 190
 Ser Phe Val Arg Ser Pro Ala Asp Ala Glu Leu Val His Lys Ile Met
 195 200 205
 Asp Glu Glu Gly Arg Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro
 210 215 220
 Glu Ala Val Thr Ser Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val
 225 230 235 240

Met Val Ala Arg Gly Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val
245 250 255

Pro Leu Val Gln Lys Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys
260 265 270

Pro Val Ile Val Ala Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser
275 280 285

Arg Pro Thr Arg Ala Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp
290 295 300

Gly Ala Asp Ala Val Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp
305 310 315 320

Pro His Asn Val Val Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu
325 330 335

Thr Asp Gly Arg Val Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg
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Gly Val Ile Ser Tyr Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala
355 360 365

Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val
370 375 380

Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu
385 390 395 400

Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu
405 410 415

Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg
420 425 430

Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val
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Val Ala Gly Ser Pro Pro Gly Val Thr Gly Asn Thr Asn Met Ile His
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1957)

<223> RXN02675

<400> 75

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											1					5		
cag	gac	att	ctc	cag	gag	atc	aag	act	gaa	ctc	gac	gag	tta	att	cta	163		
Gln	Asp	Ile	Leu	Gln	Glu	Ile	Lys	Thr	Glu	Leu	Asp	Glu	Leu	Ile	Leu			
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gaa	ctt	gat	gag	gtg	aca	caa	act	cac	agc	gag	gcc	atc	ggg	cag	gtc	211		
Glu	Leu	Asp	Glu	Val	Thr	Gln	Thr	His	Ser	Glu	Ala	Ile	Gly	Gln	Val			
				25					30					35				
tcc	cca	acc	cat	tac	gtt	ggc	gcc	cgc	aac	ctc	atg	cat	tac	gcg	cat	259		
Ser	Pro	Thr	His	Tyr	Val	Gly	Ala	Arg	Asn	Leu	Met	His	Tyr	Ala	His			
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ctt	cgc	acc	aaa	gac	ctc	cgt	ggc	ctg	cag	caa	cgc	ctc	tcc	tct	gtg	307		
Leu	Arg	Thr	Lys	Asp	Leu	Arg	Gly	Leu	Gln	Gln	Arg	Leu	Ser	Ser	Val			
				55					60					65				
gga	gct	acc	cgc	ttg	act	acc	acc	gaa	cca	gca	gtg	cag	gcc	cgc	ctc	355		
Gly	Ala	Thr	Arg	Leu	Thr	Thr	Thr	Glu	Pro	Ala	Val	Gln	Ala	Arg	Leu			
				70					75					80				
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Lys	Ala	Ala	Arg	Asn	Val	Ile	Gly	Ala	Phe	Ala	Gly	Glu	Gly	Pro	Leu			
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Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	Asp	Ala	Asp	Glu	Ile			
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Leu	Asp	Glu	His	Ala	Glu	Ile	Leu	Leu	Gly	Glu	Pro	Leu	Pro	Asp	Thr			
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cca	tcc	tgc	atc	atg	gtc	acc	ctg	ccc	acc	gaa	gcc	gcc	acc	gac	att	547		
Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu	Ala	Ala	Thr	Asp	Ile			
				135					140					145				
gaa	ctt	gtc	cgt	ggc	ttc	gcc	aaa	agc	ggc	atg	aat	cta	gct	cgc	atc	595		
Glu	Leu	Val	Arg	Gly	Phe	Ala	Lys	Ser	Gly	Met	Asn	Leu	Ala	Arg	Ile			
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aac	tgt	gca	cac	gac	gat	gaa	acc	gtc	tgg	aag	cag	atg	atc	gac	aac	643		
Asn	Cys	Ala	His	Asp	Asp	Glu	Thr	Val	Trp	Lys	Gln	Met	Ile	Asp	Asn			
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gtc	cac	acc	gtt	gca	gaa	gaa	gtt	ggc	cgg	gaa	atc	cgc	gtc	agc	atg	691		
Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu	Ile	Arg	Val	Ser	Met			
				185					190					195				
gac	ctc	gcc	gga	cca	aaa	gta	cgc	acc	ggc	gaa	atc	gcc	cca	ggc	gca	739		
Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu	Ile	Ala	Pro	Gly	Ala			
				200					205					210				
gaa	gta	ggc	cgc	gca	cga	gta	acc	cgc	gac	gaa	acc	gga	aaa	gta	ctg	787		
Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu			
				215					220					225				
acg	ccc	gca	aaa	ctg	tgg	atc	acc	gcc	cac	ggc	tcc	gaa	cca	gtc	cca	835		
Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	Ser	Glu	Pro	Val	Pro			

230	235	240	245	
gcc ccc gaa agc ctg ccc ggt cgc ccc gct ctg ccg att gaa gtc acc Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu Pro Ile Glu Val Thr	250	255	260	883
cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro	265	270	275	931
gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp	280	285	290	979
ggc gcg gtc ctc gcc gaa ggc cca caa aaa gcc tac atc tcc aac ggc Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala Tyr Ile Ser Asn Gly	295	300	305	1027
acc ctc ctg gaa cac aac tac gac cgc tcc cgg gtc tac ggc atc ccc Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro	310	315	320	1075
gcc gta gtt cag cgc atc aac ctc aaa gtc ggc gac cgc ctc atc ctt Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly Asp Arg Leu Ile Leu	330	335	340	1123
acc gac gaa gaa ctc acc tac gat cca tcc ctc gga tcc ggc cgc aca Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr	345	350	355	1171
cca cgc atc agc tgc acc ctt cca caa gca gtc gat gca att aaa gtc Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val	360	365	370	1219
ggg cac cgc gtg ctt ttc gac gac gga gcc atc gcc gca gtc tgc atc Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile Ala Ala Val Cys Ile	375	380	385	1267
gac aag acc tcc act gcc gac ggc cac aac gac gta gaa ttg gaa gtc Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val	390	395	400	1315
acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile	410	415	420	1363
aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp	425	430	435	1411
ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile	440	445	450	1459
tcc ttc atc cga aaq gtc gcc gac gtg gaa tac ctc ctc caa gca ctc Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu	455	460	465	1507
gcc gac atc gga gat cca gta gcc gtc gaa cgc ctt ggc ctc gtc ctt Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg Leu Gly Leu Val Leu	470	475	480	1555
				485

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aaa atc gag acc atc cca ggc tac gaa ggc ctc gcc caa atc ctc ctg 1603
Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu Ala Gln Ile Leu Leu
                     490                     495                     500

acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc cgc gga gac 1651
Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala Arg Gly Asp
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ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc ccc caa ctg 1699
Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val Pro Gln Leu
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atc atg gcc ctt gcc gaa gcc gcc cac gtc cca acc atc ttg gcc acc 1747
Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile Leu Ala Thr
                     535                     540                     545

caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct cgc gca gaa 1795
Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser Arg Ala Glu
550                     555                     560                     565

atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc atg ctg aac 1843
Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val Met Leu Asn
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aag gga cca cac atc aac gac gcc atc aag gtc ctc acc gaa atg agc 1891
Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser
                     585                     590                     595

cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg ctg cgc aag 1939
Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys
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Val Lys Ser Trp Glu Glu
615

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<213> Corynebacterium glutamicum

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Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
35                     40                     45

Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
50                     55                     60

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
65                     70                     75                     80

Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
85                     90                     95

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Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
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 Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
 115 120 125
 Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
 130 135 140
 Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
 145 150 155 160
 Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
 165 170 175
 Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
 180 185 190
 Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
 195 200 205
 Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
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 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
 225 230 235 240
 Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
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 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
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 Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
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 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
 305 310 315 320
 Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
 325 330 335
 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
 340 345 350
 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
 355 360 365
 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
 370 375 380
 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
 385 390 395 400
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
 405 410 415

Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
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Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
 435 440 445

Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
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Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg
 465 470 475 480

Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu
 485 490 495

Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
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Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
 515 520 525

Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro
 530 535 540

Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
 545 550 555 560

Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
 565 570 575

Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
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Leu Thr Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg
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<223> FRXA02675

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cgc gga gac ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc 96
 Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
 20 25 30

ccc caa ctg atc atg gcc ctt gca gaa gcc gcc cac gtc cca acc atc 144
 Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile

35	40	45	
ttg gcc acc caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct			192
Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser			
50	55	60	
cgc gca gaa atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc			240
Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val			
65	70	75	80
atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc			288
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr			
	85	90	95
gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg			336
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu			
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Leu Arg Lys Val Lys Ser Trp Glu Glu			
	115	120	
cgt			386

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 Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile
 35 40 45
 Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
 50 55 60
 Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
 65 70 75 80
 Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
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 Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu
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 Leu Arg Lys Val Lys Ser Trp Glu Glu
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<223> FRXA02695

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                                         Met Asn Glu Phe Asp
                                         1      5

cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta 163
Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
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gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc 211
Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
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tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat 259
Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
                        40                        45                        50

ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg 307
Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val
                        55                        60                        65

gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc 355
Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
                        70                        75                        80                        85

aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt 403
Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu
                        90                        95                        100

tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att 451
Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile
                        105                        110                        115

ctc gac gag cac gcc gaa att ctc ctt ggc gaa ccc cta ccg gat act 499
Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr
                        120                        125                        130

cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att 547
Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile
                        135                        140                        145

gaa ctt gtc cgt ggc ttc gcc aaa agc ggc atg aat cta gct cgc atc 595
Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile
150                        155                        160                        165

aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac 643
Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn
                        170                        175                        180

gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg 691
Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met
                        185                        190                        195

gac ctc gcc gga cca aaa gta cgc acc ggc gaa atc gcc cca ggc gca 739

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Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu	Ile	Ala	Pro	Gly	Ala		
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gaa	gta	ggg	cgc	gca	cga	gta	acc	cgc	gac	gaa	acc	gga	aaa	gta	ctg	787	
Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu		
	215					220					225						
acg	ccc	gca	aaa	ctg	tgg	atc	acc	gcc	cac	ggc	tcc	gaa	cca	gtc	cca	835	
Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	Ser	Glu	Pro	Val	Pro		
	230				235					240				245			
gcc	ccc	gaa	agc	ctg	ccc	ggg	cgc	ccc	gct	ctg	ccg	att	gaa	gtc	acc	883	
Ala	Pro	Glu	Ser	Leu	Pro	Gly	Arg	Pro	Ala	Leu	Pro	Ile	Glu	Val	Thr		
				250					255					260			
cca	gaa	tgg	ttc	gac	aaa	cta	gaa	atc	ggc	agc	gtc	atc	aac	gtc	cca	931	
Pro	Glu	Trp	Phe	Asp	Lys	Leu	Glu	Ile	Gly	Ser	Val	Ile	Asn	Val	Pro		
			265					270					275				
gac	acc	cgc	gga	tcc	cgc	cga	gca	ttc	acc	gtg	acc	agg	gtt	ttt	gat	979	
Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val	Thr	Arg	Val	Phe	Asp		
			280				285					290					
ggc	gcg	gtc	ctc	gcc	gaa	ggc	cca	caa	aaa	gcc	tac	atc	tcc	aac	ggc	1027	
Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala	Tyr	Ile	Ser	Asn	Gly		
	295					300					305						
acc	ctc	ctg	gaa	cac	aac	tac	gac	cgc	tcc	cgg	gtc	tac	ggc	atc	ccc	1075	
Thr	Leu	Leu	Glu	His	Asn	Tyr	Asp	Arg	Ser	Arg	Val	Tyr	Gly	Ile	Pro		
	310				315					320					325		
gcc	gta	gtt	cag	cgc	atc	aac	ctc	aaa	gtc	ggc	gac	cgc	ctc	atc	ctt	1123	
Ala	Val	Val	Gln	Arg	Ile	Asn	Leu	Lys	Val	Gly	Asp	Arg	Leu	Ile	Leu		
				330					335					340			
acc	gac	gaa	gaa	ctc	acc	tac	gat	cca	tcc	ctc	gga	tcc	ggc	cgc	aca	1171	
Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu	Gly	Ser	Gly	Arg	Thr		
			345					350					355				
cca	cgc	atc	agc	tgc	acc	ctt	cca	caa	gca	gtc	gat	gca	att	aaa	gtc	1219	
Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val	Asp	Ala	Ile	Lys	Val		
			360				365					370					
ggg	cac	cgc	gtg	ctt	ttc	gac	gac	gga	gcc	atc	ggc	gca	gtc	tgc	atc	1267	
Gly	His	Arg	Val	Leu	Phe	Asp	Asp	Gly	Ala	Ile	Ala	Ala	Val	Cys	Ile		
	375					380					385						
gac	aag	acc	tcc	act	gcc	gac	ggc	cac	aac	gac	gta	gaa	ttg	gaa	gtc	1315	
Asp	Lys	Thr	Ser	Thr	Ala	Asp	Gly	His	Asn	Asp	Val	Glu	Leu	Glu	Val		
	390				395					400				405			
acc	cac	gcc	cgc	cca	caa	ggc	gta	aac	ctg	gcc	gca	tac	aag	gga	atc	1363	
Thr	His	Ala	Arg	Pro	Gln	Gly	Val	Asn	Leu	Ala	Ala	Tyr	Lys	Gly	Ile		
				410				415						420			
aac	ctc	cca	gac	tcc	gaa	ctt	cca	ctc	cca	agc	ctc	act	gaa	gaa	gac	1411	
Asn	Leu	Pro	Asp	Ser	Glu	Leu	Pro	Leu	Pro	Ser	Leu	Thr	Glu	Glu	Asp		
			425					430					435				
ctc	caa	cac	ctg	cgc	ttt	gtc	gtc	aaa	tac	gcc	gac	atc	gca	gcc	atc	1459	
Leu	Gln	His	Leu	Arg	Phe	Val	Val	Lys	Tyr	Ala	Asp	Ile	Ala	Ala	Ile		

440 445 450
 tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc 1507
 Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu
 455 460 465

 gcc gac atc gga gat 1522
 Ala Asp Ile Gly Asp
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 Asp Glu Leu Ile Leu Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu
 20 25 30
 Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
 35 40 45
 Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
 50 55 60
 Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65 70 75 80
 Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
 85 90 95
 Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
 100 105 110
 Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
 115 120 125
 Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
 130 135 140
 Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
 145 150 155 160
 Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
 165 170 175
 Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
 180 185 190
 Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
 195 200 205
 Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
 210 215 220
 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
 225 230 235 240

Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
 245 250 255
 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
 260 265 270
 Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
 275 280 285
 Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
 290 295 300
 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
 305 310 315 320
 Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
 325 330 335
 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
 340 345 350
 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
 355 360 365
 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
 370 375 380
 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
 385 390 395 400
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
 405 410 415
 Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
 420 425 430
 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
 435 440 445
 Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
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<220>
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 <223> RXA00682

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	Met	Ala	Asn	Lys	Ser	
	1				5	
ttc ccc aag ccc tcc gat ctt cca gtg ccc aag ggc gct gaa ggt tgg						163
Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys Gly Ala Glu Gly Trp						
	10				20	
gaa gat ctg tac ccg tac tac ctc gtt ttc caa gac aag ctc atg gat						211
Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln Asp Lys Leu Met Asp						
	25				35	
caa gag aat gag aaa ttc tgg ttc tgc gat tca cag cac tgg cca act						259
Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser Gln His Trp Pro Thr						
	40				50	
gtg ttc aag cct ttt gaa act atc ggt ggt gaa ttc gct gta aag tgc						307
Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu Phe Ala Val Lys Cys						
	55				65	
ctc ggc caa tac aac gct cgg cat ttg atg atc ccg aat gcc aat ggc						355
Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile Pro Asn Ala Asn Gly						
	70				80	85
atc gag ttc cgc gtg cat ctg gga tac ctc tat atg tcc cct att cca						403
Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr Met Ser Pro Ile Pro						
	90				95	100
gtg cct gaa gat cag att gcg gaa cgc gtc ccc atg ttc cag gaa cgc						451
Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro Met Phe Gln Glu Arg						
	105				110	115
atc acg cac tac ttc caa aac tgg gag cca atg ctg gca aat tgg aag						499
Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met Leu Ala Asn Trp Lys						
	120				125	130
gag cga gta tta gga acc atc aat gag ctg gaa tct cta gaa ttc aag						547
Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu Ser Leu Glu Phe Lys						
	135				140	145
cca ctg cct gac tac gtg cct atc gat gat att gtc tcc gga aaa gcc						595
Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile Val Ser Gly Lys Ala						
	150				155	160
aaa gac ggc acc gaa gta ctc atg gaa aac ttc gat cgg ctc att cag						643
Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe Asp Arg Leu Ile Gln						
	170				175	180
ctc gcc tac caa aac tgg caa tac cac ttt gag ttc ctc aac ttg ggt						691
Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu Phe Leu Asn Leu Gly						
	185				190	195
tac atc gct tac cta gat ttc ttc aat ttc tgc aag gaa gtc ttc cca						739
Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys Lys Glu Val Phe Pro						
	200				205	210
gat atc cct gat caa tca att tcg atg atg gtt cag ggc gtg gat atg						787
Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val Gln Gly Val Asp Met						
	215				220	225
gag ctg ttc cgc ccc gat gat gaa cta aag att ctg gca cag cta gcg						835
Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile Leu Ala Gln Leu Ala						

230	235	240	245	
gtc gac ctt ggc ctg caa act cac ttt gcc aac ccg gat gat ccg caa	883			
Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn Pro Asp Asp Pro Gln				
250	255	260		
gct acc ttg gct gct atc gca aag gca gaa ggc ggc gcg aca tgg ata	931			
Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly Gly Ala Thr Trp Ile				
265	270	275		
gcg cgc tgg gaa gaa gca caa gat ccg tgg ttc aac ttc acc gtc ggt	979			
Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe Asn Phe Thr Val Gly				
280	285	290		
aat ggc ttc tac ggt cac gat aaa tac tgg atc gag cac ctg gaa ctt	1027			
Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile Glu His Leu Glu Leu				
295	300	305		
cca ctg ggg tac atc gcg gat tac atc cgc cgc cta gat gaa ggc caa	1075			
Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg Leu Asp Glu Gly Gln				
310	315	320	325	
acc atc tcc cgc ccg aaa gat gaa ctc atc gca gaa aag gaa cgc gtg	1123			
Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala Glu Lys Glu Arg Val				
330	335	340		
gtg gaa gaa tac cgc gac ctt ttg gat gga gaa caa ctc gcg cag ttt	1171			
Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu Gln Leu Ala Gln Phe				
345	350	355		
gat gct aaa tgc ggc ctc gct gct act gca tac ccc tat gtg gaa aac	1219			
Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr Pro Tyr Val Glu Asn				
360	365	370		
cat aac ttc tac atc gag cac tgg acc atg tca gta ttt tgg cgc aaa	1267			
His Asn Phe Tyr Ile Glu His Trp Thr Met Ser Val Phe Trp Arg Lys				
375	380	385		
gta cgc gaa ctt tcc cgc act ctc cag ggc tac ggt ttc tgg gag aac	1315			
Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr Gly Phe Trp Glu Asn				
390	395	400	405	
gag gat gac atg ttg tac ctc aac cgc act gaa gtc cgc gat gtc ctc	1363			
Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu Val Arg Asp Val Leu				
410	415	420		
ttc gac ctg gct act gcg tgg ggt gtc ggc gca ccc ggt ggt cca att	1411			
Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala Pro Gly Gly Pro Ile				
425	430	435		
ggc acg atc att tgg ccg gaa gaa att gag cga aga aaa gca att gtc	1459			
Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg Arg Lys Ala Ile Val				
440	445	450		
acc gct ttg aaa act gcc cga cca gcg cca gct ctt aac act cct cca	1507			
Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala Leu Asn Thr Pro Pro				
455	460	465		
gag tcc atc acc gaa cct ttc acc cgc atg ctc tgg gga atc acc acc	1555			
Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu Trp Gly Ile Thr Thr				
470	475	480	485	

gaa cag gtg caa tca tgg ttg ggc aat gac gag gat gcc gaa gaa gga 1603
 Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu Asp Ala Glu Glu Gly
 490 495 500

acc ctt aaa ggc atg gct gca tcc cct ggt gtg gtg gaa ggc tac gct 1651
 Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val Val Glu Gly Tyr Ala
 505 510 515

cga gta att ctc agc gca gat gac ctt tca gaa atc cag cag gat gaa 1699
 Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu Ile Gln Gln Asp Glu
 520 525 530

atc ctc gtt gcc cct gta aca gca cct tct tgg ggc cca atc ttt ggc 1747
 Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp Gly Pro Ile Phe Gly
 535 540 545

aaa atc aag gca aca gtc act gat att ggt ggc atg atg agc cat gct 1795
 Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly Met Met Ser His Ala
 550 555 560 565

gcg atc gtg tgc cgc gaa tac ggc ttg ccg gct gtt act gga act ggc 1843
 Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala Val Thr Gly Thr Gly
 570 575 580

gct gca tcc acc acc atc aaa acc ggc gat tac ctc aag gtc gat gga 1891
 Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr Leu Lys Val Asp Gly
 585 590 595

acc aag ggc aag gtt gtc att gtt gat cca gat gcg cca cgc atc gaa 1939
 Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu
 600 605 610

gga ccc ggc gcg cac agc cat gcg cac tca gta gca gca cat ggg gtg 1987
 Gly Pro Gly Ala His Ser His Ala His Ser Val Ala Ala His Gly Val
 615 620 625

gat aca cat gcc tagtccacgc actgttctta tca 2022
 Asp Thr His Ala
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<210> 82

<211> 633

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Ala Asn Lys Ser Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys
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Gly Ala Glu Gly Trp Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln
 20 25 30

Asp Lys Leu Met Asp Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser
 35 40 45

Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu
 50 55 60

Phe Ala Val Lys Cys Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile

65	70	75	80
Pro Asn Ala Asn Gly Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr	85	90	95
Met Ser Pro Ile Pro Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro	100	105	110
Met Phe Gln Glu Arg Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met	115	120	125
Leu Ala Asn Trp Lys Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu	130	135	140
Ser Leu Glu Phe Lys Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile	145	150	155
Val Ser Gly Lys Ala Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe	165	170	175
Asp Arg Leu Ile Gln Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu	180	185	190
Phe Leu Asn Leu Gly Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys	195	200	205
Lys Glu Val Phe Pro Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val	210	215	220
Gln Gly Val Asp Met Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile	225	230	235
Leu Ala Gln Leu Ala Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn	245	250	255
Pro Asp Asp Pro Gln Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly	260	265	270
Gly Ala Thr Trp Ile Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe	275	280	285
Asn Phe Thr Val Gly Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile	290	295	300
Glu His Leu Glu Leu Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg	305	310	315
Leu Asp Glu Gly Gln Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala	325	330	335
Glu Lys Glu Arg Val Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu	340	345	350
Gln Leu Ala Gln Phe Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr	355	360	365
Pro Tyr Val Glu Asn His Asn Phe Tyr Ile Glu His Trp Thr Met Ser	370	375	380
Val Phe Trp Arg Lys Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr	385	390	395
			400

Gly Phe Trp Glu Asn Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu
 405 410 415

Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala
 420 425 430

Pro Gly Gly Pro Ile Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg
 435 440 445

Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala
 450 455 460

Leu Asn Thr Pro Pro Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu
 465 470 475 480

Trp Gly Ile Thr Thr Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu
 485 490 495

Asp Ala Glu Glu Gly Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val
 500 505 510

Val Glu Gly Tyr Ala Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu
 515 520 525

Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp
 530 535 540

Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly
 545 550 555 560

Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala
 565 570 575

Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr
 580 585 590

Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp
 595 600 605

Ala Pro Arg Ile Glu Gly Pro Gly Ala His Ser His Ala His Ser Val
 610 615 620

Ala Ala His Gly Val Asp Thr His Ala
 625 630

<210> 83

<211> 1215

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1192)

<223> RXA00683

<400> 83

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gacttgaac gcttaacgct ttattaaata aggagacacc atg acc aac agt ttg 115

230	235	240	245	
gtc tcc gaa cac att gga agc aaa cac gct gaa ctc atc ccc gat gcc				883
Val Ser Glu His Ile Gly Ser Lys His Ala Glu Leu Ile Pro Asp Ala				
	250	255	260	
acc agt gga agc ctc gtg gaa aag ccc gtt gat gaa gaa cgc gca aac				931
Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp Glu Glu Arg Ala Asn				
	265	270	275	
cgc cgc agt ctg act gat gag gaa atg ctc gct gtg gca caa atg gct				979
Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala Val Ala Gln Met Ala				
	280	285	290	
aag cgt gca gaa aaa cac tac aag tgc cca caa gat atc gaa tgg gcg				1027
Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln Asp Ile Glu Trp Ala				
	295	300	305	
ctg gac gct gat ctg cca gat gga gaa aac ctt ctg tta ttg caa tcc				1075
Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu Leu Leu Leu Gln Ser				
	310	315	320	325
cgc ccg gaa act atc cac tcc aac ggt gtg aag aag gaa acc cca act				1123
Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys Lys Glu Thr Pro Thr				
	330	335	340	
ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc				1171
Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr				
	345	350	355	
gtc gca atg acc ggc acg aag taaaaccacc gcaccttttc gtc				1215
Val Ala Met Thr Gly Thr Lys				
	360			

<210> 84

<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

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Leu Asp Pro Val Leu Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val
20 25 30

Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr
35 40 45

Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His
50 55 60

Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val
65 70 75 80

Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val
85 90 95

Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met
100 105 110

Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr
 115 120 125
 Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr
 130 135 140
 Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys
 145 150 155 160
 Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn
 165 170 175
 Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met
 180 185 190
 Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn
 195 200 205
 Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu
 210 215 220
 Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys
 225 230 235 240
 Ile Thr Leu Gln Val Val Ser Glu His Ile Gly Ser Lys His Ala Glu
 245 250 255
 Leu Ile Pro Asp Ala Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp
 260 265 270
 Glu Glu Arg Ala Asn Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala
 275 280 285
 Val Ala Gln Met Ala Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln
 290 295 300
 Asp Ile Glu Trp Ala Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu
 305 310 315 320
 Leu Leu Leu Gln Ser Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys
 325 330 335
 Lys Glu Thr Pro Thr Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp
 340 345 350
 Phe Ser Ser Ile Thr Val Ala Met Thr Gly Thr Lys
 355 360

<210> 85
 <211> 1860
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1837)
 <223> RXN00635

<400> 85

ctggcagggcg ggcgaagcgt ggcaacaact ggaattttaag agcacaattg aagtcgcacc 60

aagtttaggca acacaatagc cataacgttg aggagttcag atg gca cac agc tac 115
Met Ala His Ser Tyr
1 5

gca gaa caa tta att gac act ttg gaa gct caa ggt gtg aag cga att 163
Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile
10 15 20

tat ggt ttg gtg ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc 211
Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg
25 30 35

caa tca gat att gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg 259
Gln Ser Asp Ile Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala
40 45 50

ttt gca gcc ggt gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt 307
Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys
55 60 65

gct gct tct tgt ggt cct gga aac aca cac ctg att cag ggt ctt tat 355
Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr
70 75 80 85

gat tcg cat cga aat ggt gcg aag gtg ttg gcc atc gct agc cat att 403
Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile
90 95 100

ccg agt gcc cag att ggt tcg acg ttc ttc cag gaa acg cat ccg gag 451
Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu
105 110 115

att ttg ttt aag gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt 499
Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly
120 125 130

gag cag ggt gaa cgc att ttg cat cac gcg att cag tcc acc atg gcg 547
Glu Gln Gly Glu Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala
135 140 145

ggt aaa ggt gtg tcg gtg gta gtg att cct ggt gat atc gct aag gaa 595
Gly Lys Gly Val Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu
150 155 160 165

gac gca ggt gac ggt act tat tcc aat tcc act att tct tct ggc act 643
Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr
170 175 180

cct gtg gtg ttc ccg gat cct act gag gct gca gcg ctg gtg gag gcg 691
Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala
185 190 195

att aac aac gct aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag 739
Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys
200 205 210

aat gct cgc gcg cag gtg ttg gag ttg gcg gag aag att aaa tca ccg 787
Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro
215 220 225

atc ggg cat gcg ctg ggt ggt aag cag tac atc cag cat gag aat ccg Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro 230 235 240 245	835
ttt gag gtc ggc atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp 250 255 260	883
gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro 265 270 275	931
tat tct gat ttc ctt cct aaa gac aac gtt gcc cag gtg gat atc aac Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn 280 285 290	979
ggt gcg cac att ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly 295 300 305	1027
gat gtt gct gca aca atc gaa aat att ttg cct cat gtg aag gaa aaa Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys 310 315 320 325	1075
aca gat cgt tcc ttc ctt gat cgg atg ctc aag gca cac gag cgt aag Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys 330 335 340	1123
ttg agc tcg gtg gta gag acg tac aca cat aac gtc gag aag cat gtg Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val 345 350 355	1171
cct att cac cct gaa tac gtt gcc tct att ttg aac gag ctg gcg gat Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp 360 365 370	1219
aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His 375 380 385	1267
gcg agg tac atc gag aat ccg gag gga acg cgc gac ttt gtg ggt tca Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser 390 395 400 405	1315
ttc cgc cac ggc acg atg gct aat gcg ttg cct cat gcg att ggt gcg Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala 410 415 420	1363
caa agt gtt gat cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly 425 430 435	1411
ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln 440 445 450	1459
ctt ccg ctg aag gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val 455 460 465	1507

aag ttg gag atg ctc gtg gag gga cag cca gaa ttt ggt act gac cat 1555
Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His
470 475 480 485

gag gaa gtg aat ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg 1603
Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser
490 495 500

gta cgc atc acc gat ccg aag aaa gtt cgc gag cag cta gct gag gca 1651
Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala
505 510 515

ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat 1699
Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn
520 525 530

gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc 1747
Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe
535 540 545

agc aag gcg gcc acc cga acc gtc ttt ggt gga gga gta gga gcg atg 1795
Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met
550 555 560 565

atc gat ctg gcc cgt tcg aac ata agg aat att cct act cca 1837
Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
570 575

tgatgattga tacacctgct gtt 1860

<210> 86

<211> 579

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
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Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
20 25 30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
35 40 45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
50 55 60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
65 70 75 80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
85 90 95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
100 105 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
115 120 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
 130 135 140
 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
 145 150 155 160
 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
 165 170 175
 Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
 180 185 190
 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
 195 200 205
 Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
 210 215 220
 Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
 225 230 235 240
 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
 245 250 255
 Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
 260 265 270
 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
 275 280 285
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 290 295 300
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 305 310 315 320
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 325 330 335
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 340 345 350
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 355 360 365
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 370 375 380
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 385 390 395 400
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 405 410 415
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 420 425 430
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 435 440 445
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser

450 455 460
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 465 470 475 480
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 485 490 495
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 500 505 510
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 515 520 525
 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 530 535 540
 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
 545 550 555 560
 Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
 565 570 575
 Pro Thr Pro

<210> 87
 <211> 552
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (88)..(552)
 <223> FRXA02807

<400> 87
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 caatagccat aacgttgagg agttcagatg gca cac agc tac gca gaa caa tta 114
 Met Ala His Ser Tyr Ala Glu Gln Leu
 1 5
 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 162
 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 10 15 20 25
 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 210
 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 30 35 40
 gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 258
 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
 45 50 55
 gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 306
 Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
 60 65 70
 ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga 354

Gly	Pro	Gly	Asn	Thr	His	Leu	Ile	Gln	Gly	Leu	Tyr	Asp	Ser	His	Arg	
	75					80					85					
aat	ggt	gcg	aag	gtg	ttg	gcc	atc	gct	agc	cat	att	ccg	agt	gcc	cag	402
Asn	Gly	Ala	Lys	Val	Leu	Ala	Ile	Ala	Ser	His	Ile	Pro	Ser	Ala	Gln	
90					95					100					105	
att	ggt	tcg	acg	ttc	ttc	cag	gaa	acg	cat	ccg	gag	att	ttg	ttt	aag	450
Ile	Gly	Ser	Thr	Phe	Phe	Gln	Glu	Thr	His	Pro	Glu	Ile	Leu	Phe	Lys	
				110					115					120		
gaa	tgc	tct	ggt	tac	tgc	gag	atg	gtg	aat	ggt	ggt	gag	cag	ggt	gaa	498
Glu	Cys	Ser	Gly	Tyr	Cys	Glu	Met	Val	Asn	Gly	Gly	Glu	Gln	Gly	Glu	
			125					130					135			
cgc	att	ttg	cat	cac	gcg	att	cag	tcc	acc	atg	gcg	ggt	aaa	ggt	gtg	546
Arg	Ile	Leu	His	His	Ala	Ile	Gln	Ser	Thr	Met	Ala	Gly	Lys	Gly	Val	
		140					145					150				
tcg	gtg															552
Ser	Val															
	155															

<210> 88
 <211> 155
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 88
 Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
 1 5 10 15
 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
 20 25 30
 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
 35 40 45
 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
 50 55 60
 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 65 70 75 80
 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
 85 90 95
 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
 100 105 110
 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
 115 120 125
 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
 130 135 140
 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val
 145 150 155

<210> 89
 <211> 944
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(921)
 <223> FRXA00635

<400> 89
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 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
 1 5 10 15
 cag gtg gat atc aac ggt gcg cac att ggt cga cgt acc acg gtg aag 96
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 20 25 30
 tat ccg gtg acc ggt gat gtt gct gca aca atc gaa aat att ttg cct 144
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 35 40 45
 cat gtg aag gaa aaa aca gat cgt tcc ttc ctt gat cgg atg ctc aag 192
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 50 55 60
 gca cac gag cgt aag ttg agc tcg gtg gta gag acg tac aca cat aac 240
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 65 70 75 80
 gtc gag aag cat gtg cct att cac cct gaa tac gtt gcc tct att ttg 288
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 85 90 95
 aac gag ctg gcg gat aag gat gcg gtg ttt act gtg gat acc ggc atg 336
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 100 105 110
 tgc aat gtg tgg cat gcg agg tac atc gag aat ccg gag gga acg cgc 384
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 115 120 125
 gac ttt gtg ggt tca ttc cgc cac ggc acg atg gct aat gcg ttg cct 432
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140
 cat gcg att ggt gcg caa agt gtt gat cga aac cgc cag gtg atc gcg 480
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160
 atg tgt ggc gat ggt ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc 528
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175
 gtt aag ctg cac caa ctt ccg ctg aag gct gtg gtg ttt aac aac agt 576
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190
 tct ttg ggc atg gtg aag ttg gag atg ctc gtg gag gga cag cca gaa 624
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu

195	200	205	
ttt ggt act gac cat gag gaa gtg aat ttc gca gag att gcg gcg gct			672
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala			
210	215	220	
gcg ggt atc aaa tcg gta cgc atc acc gat ccg aag aaa gtt cgc gag			720
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu			
225	230	235	240
cag cta gct gag gca ttg gca tat cct gga cct gta ctg atc gat atc			768
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile			
245	250	255	
gtc acg gat cct aat gcg ctg tcg atc cca cca acc atc acg tgg gaa			816
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu			
260	265	270	
cag gtc atg gga ttc agc aag gcg gcc acc cga acc gtc ttt ggt gga			864
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly			
275	280	285	
gga gta gga gcg atg atc gat ctg gcc cgt tcg aac ata agg aat att			912
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile			
290	295	300	
cct act cca tgatgattga tacacctgct gtt			944
Pro Thr Pro			
305			

<210> 90

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
1 5 10 15

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
20 25 30

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
35 40 45

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
50 55 60

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
65 70 75 80

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
85 90 95

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
100 105 110

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
115 120 125

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 195 200 205
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 210 215 220
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 225 230 235 240
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 245 250 255
 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 260 265 270
 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
 275 280 285
 Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
 290 295 300
 Pro Thr Pro
 305

<210> 91
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXN03044

<400> 91.
 tacgccaccc acggcaaggc catgattccg ctgtacatct tctactcgat gttcgggatt 60
 ccagcgcacc ggtgactcca tctgggcagc agccgatcag atg gca cgt ggc ttc 115
 Met Ala Arg Gly Phe
 1 5
 ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc 163
 Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
 10 15 20
 cag cac atg gat gga cac tcc cct gtc ttg gct tcc acc aac gag ggt 211
 Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
 25 30 35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt	259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val	
40 45 50	
cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt	307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val	
55 60 65	
atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag	355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu	
70 75 80 85	
cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac	403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr	
90 95 100	
tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt	451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly	
105 110 115	
gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac	499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp	
120 125 130	
tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg	547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu	
135 140 145	
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt	595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly	
150 155 160 165	
gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc	643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser	
170 175 180	
ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag	691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln	
185 190 195	
atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc	739
Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly	
200 205 210	
ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc	787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile	
215 220 225	
gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa	835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu	
230 235 240 245	
ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag	883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys	
250 255 260	
ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa	931
Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu	
265 270 275	

taaatacacct caagggacag ata

954

<210> 92

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

Met Ala Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu
 1 5 10 15

Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala
 20 25 30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
 165 170 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
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Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
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Asn Ala Pro Glu Glu

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 <223> FRXA02852

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 tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30
 tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80
 cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
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<210> 94
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 94
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 20 25 30
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

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1 5	
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10 15 20	
cag cac atg gat gga cac tcc cct gtt ttg gct tcc acc aac gag ggt Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly	211
25 30 35	
gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val	259
40 45 50	
cac cgt ggc atc gac cgc atg tac gcc cca gcc aag ggt gaa gat gtt His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val	307
55 60 65	
atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu	355
70 75 80 85	
cca gaa gga ctg gac gta gaa gcc ctg cac aag gcc atc tac ctc tac Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr	403
90 95 100	
tcc cgc ggt gaa gcc acc gcc cat gag gca aac atc ttg gct tcc ggt Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly	451
105 110 115	
gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp	499
120 125 130	
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135 140 145	
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly	595
150 155 160 165	

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ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag 691
 Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
 185 190 195

atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc 739
 Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
 200 205 210

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 Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
 215 220 225

gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa 835
 Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
 230 235 240 245

ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag 883
 Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
 250 255 260

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa 931
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<211> 277

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
 165 170 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240

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Asn Ala Pro Glu Glu
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 <212> DNA
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 Met Ala Asp Gln Ala
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aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65
 cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70 75 80 85
 cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
 90 95 100
 cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
 105 110 115
 gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
 Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
 120 125 130
 ggc gca gcc 508
 Gly Ala Ala
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
 100 105 110
 Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
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<212> DNA

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<223> FRXA02887

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                               Met Ala Asp Gln Ala
                               1 5
aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
          10          15          20
gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
          25          30          35
gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
          40          45          50
cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
          55          60          65
cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
          70          75          80          85
cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
          90          95          100
cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
          105          110          115
gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
          120          125          130
ggc gca gcc
Gly Ala Ala 508
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<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

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 Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
 100 105 110
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 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30
 act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336

Phe Val Val	Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly	
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Asn Thr Lys Ile Ile Gln Glu Leu Ser Phe Phe Arg Gly Ala Gly		
115	120	125
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Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu		
130	135	140
gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc	480	
Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser		
145	150	155
gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt	528	
Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg		
165	170	175
gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac	576	
Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn		
180	185	190
atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac	624	
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr		
195	200	205
cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc	672	
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg		
210	215	220
cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac	720	
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His		
225	230	235
aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt	768	
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu		
245	250	255
gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat	816	
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp		
260	265	270
gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt	864	
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly		
275	280	285
gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc	912	
Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu		
290	295	300
ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt	960	
Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val		
305	310	315
cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag	1008	
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln		
325	330	335
cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg	1056	
Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met		

340	345	350	
cgc gat aag ggc ttg gct gat	cgc ctt gtc cca atc att cct gat gag	1104	
Arg Asp Lys Gly Leu Ala Asp	Arg Leu Val Pro Ile Ile Pro Asp Glu		
355	360 365		
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac	1152		
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr			
370 375	380		
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc	1200		
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu			
385 390	395 400		
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248		
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn			
405 410	415		
gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc tcc tac gcc	1296		
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala			
420 425	430		
acc cac ggc aag gcc atg att ccg ctg tac atc ttc tac tcg atg ttc	1344		
Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe			
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ggg att cca gcg cac cgg tgactccatc tgggcagcag ccg	1385		
Gly Ile Pro Ala His Arg			
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<211> 454

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

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35 40 45	
Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln	
50 55 60	
His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser	
65 70 75 80	
Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr	
85 90 95	
Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly	
100 105 110	
Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly	
115 120 125	

Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255
 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala
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<210> 103
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 <222> (1)..(1287)
 <223> FRXA02897

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 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
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 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45

ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
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cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80

cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95

ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110

aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc 384
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125

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 130 135 140

gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc 480
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160

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 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175

gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac 576
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190

atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac	624
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr	
195 200 205	
cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc	672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg	
210 215 220	
cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac	720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His	
225 230 235 240	
aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt	768
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu	
245 250 255	
gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat	816
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp	
260 265 270	
gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt	864
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly	
275 280 285	
gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc	912
Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu	
290 295 300	
ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt	960
Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val	
305 310 315 320	
cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag	1008
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln	
325 330 335	
cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg	1056
Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met	
340 345 350	
cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag	1104
Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu	
355 360 365	
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac	1152
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr	
370 375 380	
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc	1200
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu	
385 390 395 400	
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn	
405 410 415	
gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc	1287
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr	
420 425	

<210> 104
 <211> 429
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 104

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Pro	Ser	Tyr	Pro	His	Pro	His	Gly	Met	Lys	Asp	Phe	Trp	Glu	Phe	Pro	20	25	30	
Thr	Val	Ser	Met	Gly	Leu	Gly	Pro	Met	Asp	Ala	Ile	Tyr	Gln	Ala	Arg	35	40	45	
Phe	Asn	Arg	Tyr	Leu	Glu	Asn	Arg	Gly	Ile	Lys	Asp	Thr	Ser	Asp	Gln	50	55	60	
His	Val	Trp	Ala	Phe	Leu	Gly	Asp	Gly	Glu	Met	Asp	Glu	Pro	Glu	Ser	65	70	75	80
Arg	Gly	Leu	Ile	Gln	Gln	Ala	Ala	Leu	Asn	Asn	Leu	Asp	Asn	Leu	Thr	85	90	95	
Phe	Val	Val	Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Arg	Gly	100	105	110	
Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly	115	120	125	
Trp	Ser	Val	Ile	Lys	Val	Val	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu	130	135	140	
Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Ile	Met	Asn	Asn	Thr	Ser	145	150	155	160
Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg	165	170	175	
Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Ala	Lys	Leu	Val	Glu	Asn	180	185	190	
Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr	195	200	205	
Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg	210	215	220	
Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His	225	230	235	240
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu	245	250	255	
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp	260	265	270	
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly	275	280	285	

Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr
 420 425

<210> 105
 <211> 1133
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (88)..(1110)
 <223> RXN03083

<400> 105
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 ccagctcaca cgtgtggagg tgccttaatg gca aag agg atc gta att atc ggc 114
 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5
 ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 162
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10 15 20 25
 gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 210
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40
 acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 258
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55
 aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 306
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac	354
Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp	
75 80 85	
ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca	402
Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser	
90 95 100 105	
gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc	450
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr	
110 115 120	
aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa	498
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu	
125 130 135	
gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc	546
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro	
140 145 150	
cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg	594
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp	
155 160 165	
cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt	642
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val	
170 175 180 185	
ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc	690
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu	
190 195 200	
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac	738
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His	
205 210 215	
gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc	786
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg	
220 225 230	
gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc	834
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr	
235 240 245	
gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac	882
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr	
250 255 260 265	
ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat	930
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp	
270 275 280	
ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc	978
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile	
285 290 295	
aag gtt gac cgg tct ccc gca cca aca tcc ccg gtg tgt acg cag cag	1026
Lys Val Asp Arg Ser Pro Ala Pro Thr Ser Pro Val Cys Thr Gln Gln	
300 305 310	
gtg act gta ctg acc tat tcc cac tgg cgt ccg ttg cag cga tgc agg	1074

Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
 315 320 325

gcc gta tcg cca tgt atc acg cac tcg gtg aag gcg tgagcccat 1120
 Ala Val Ser Pro Cys Ile Thr His Ser Val Lys Ala
 330 335 340

ccgtttgaag act 1133

<210> 106

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
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Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
 35 40 45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
 50 55 60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
 100 105 110

Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
 115 120 125

Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
 130 135 140

Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
 145 150 155 160

Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
 165 170 175

Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
 180 185 190

Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
 195 200 205

Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
 210 215 220

Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
 225 230 235 240

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<211> 1518
<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA02853
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cccagctcac acgtgtggag gtgccttaatg gca aag agg atc gta att atc ggc 115
                Met Ala Lys Arg Ile Val Ile Ile Gly
                1         5

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ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 163
Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
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gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 211
Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
30 35 40

acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 259
Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
45 50 55

aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 307
Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
60 65 70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355
Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
75 80 85

ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 403
Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser

90	95	100	105	
gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc	451			
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr				
110 115 120				
aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa	499			
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu				
125 130 135				
gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc	547			
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro				
140 145 150				
cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg	595			
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp				
155 160 165				
cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt	643			
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val				
170 175 180 185				
ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc	691			
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu				
190 195 200				
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac	739			
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His				
205 210 215				
gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc	787			
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg				
220 225 230				
gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc	835			
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr				
235 240 245				
gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac	883			
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr				
250 255 260 265				
ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat	931			
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp				
270 275 280				
ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc	979			
Leu Gly Leu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile				
285 290 295				
aag gtt gac cgn gtc tcc cgc acc aac atc ccc ggt gtg tac gca gca	1027			
Lys Val Asp Arg Val Ser Arg Thr Asn Ile Pro Gly Val Tyr Ala Ala				
300 305 310				
ggt gac tgt act gac cta ttc cca ctg gcg tcc gtt gca gcg atg cag	1075			
Gly Asp Cys Thr Asp Leu Phe Pro Leu Ala Ser Val Ala Ala Met Gln				
315 320 325				
ggc cgt atc gcc atg tat cac gca ctc ggt gaa ggc gtg agc ccc atc	1123			
Gly Arg Ile Ala Met Tyr His Ala Leu Gly Glu Gly Val Ser Pro Ile				
330 335 340 345				

cgt ttg aag act gtt gcc acc gca gtg ttt acc cgc cca gag atc gca 1171
 Arg Leu Lys Thr Val Ala Thr Ala Val Phe Thr Arg Pro Glu Ile Ala 360
 350 355

gca gta ggt atc acc cat gca caa gtt gat tcc ggc gaa gtg tct gct 1219
 Ala Val Gly Ile Thr His Ala Gln Val Asp Ser Gly Glu Val Ser Ala 375
 365 370

cgc gtg att gtg ctt cct ttg gct act aac cca cgc gcc aag atg cgt 1267
 Arg Val Ile Val Leu Pro Leu Ala Thr Asn Pro Arg Ala Lys Met Arg 390
 380 385

tcc ctg cgc cac ggt ttt gtg aag ctg ttc tgc cgc cgt aac tct ggc 1315
 Ser Leu Arg His Gly Phe Val Lys Leu Phe Cys Arg Arg Asn Ser Gly 405
 395 400

ctg atc atc ggt ggt gtc gtg gtg gca ccg acc gcg tct gag ctg atc 1363
 Leu Ile Ile Gly Gly Val Val Val Ala Pro Thr Ala Ser Glu Leu Ile 425
 410 415 420

cta ccg atc gct gtg gca gtg acc aac cgt ctg aca gtt gct gat ctg 1411
 Leu Pro Ile Ala Val Ala Val Thr Asn Arg Leu Thr Val Ala Asp Leu 440
 430 435

gct gat acc ttc gcg gtg tac cca tca ttg tca ggt tcg att act gaa 1459
 Ala Asp Thr Phe Ala Val Tyr Pro Ser Leu Ser Gly Ser Ile Thr Glu 455
 445 450

gca gca cgt cag ctg gtt caa cat gat gat cta ggc taatttttct 1505
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<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

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Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
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Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
35 40 45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
50 55 60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly

100					105					110					
Val	Gly	Arg	Phe	Asp	Asp	Tyr	Asn	Thr	Lys	Gln	Thr	Thr	His	Tyr	Ile
	115						120					125			
Lys	Val	Thr	His	Ser	Asp	Gly	Ser	Glu	Glu	Thr	Val	Glu	Cys	Asp	Leu
	130					135					140				
Val	Leu	Val	Ala	Thr	Gly	Ala	Thr	Pro	Arg	Ile	Leu	Lys	Gly	Ala	Glu
145					150					155					160
Pro	Asp	Gly	Glu	Arg	Ile	Leu	Thr	Trp	Arg	Gln	Val	Tyr	Asp	Ile	Glu
				165					170					175	
Glu	Leu	Pro	Thr	His	Leu	Ile	Val	Val	Gly	Ser	Gly	Val	Thr	Gly	Ala
			180					185					190		
Glu	Phe	Val	Ser	Ala	Phe	Ala	Glu	Leu	Gly	Val	Lys	Val	Thr	Met	Val
	195						200					205			
Ala	Ser	Arg	Asp	Arg	Ile	Leu	Pro	His	Asp	Asp	Ala	Asp	Ala	Ala	Asp
	210					215					220				
Val	Leu	Glu	Thr	Val	Leu	Ala	Glu	Arg	Gly	Val	Ser	Leu	Glu	Lys	His
225					230					235					240
Ala	Arg	Val	Glu	Ser	Val	Thr	Arg	Thr	Glu	Asp	Gly	Gly	Val	Cys	Val
				245					250					255	
Arg	Thr	Ala	Asp	Gly	Arg	Glu	Ile	Tyr	Gly	Ser	His	Ala	Leu	Met	Thr
			260					265					270		
Val	Gly	Ser	Ile	Pro	Asn	Thr	Ala	Asp	Leu	Gly	Leu	Glu	Asn	Ile	Gly
	275					280						285			
Val	Glu	Leu	Ala	Pro	Ser	Gly	His	Ile	Lys	Val	Asp	Arg	Val	Ser	Arg
	290					295					300				
Thr	Asn	Ile	Pro	Gly	Val	Tyr	Ala	Ala	Gly	Asp	Cys	Thr	Asp	Leu	Phe
305				310						315					320
Pro	Leu	Ala	Ser	Val	Ala	Ala	Met	Gln	Gly	Arg	Ile	Ala	Met	Tyr	His
				325					330					335	
Ala	Leu	Gly	Glu	Gly	Val	Ser	Pro	Ile	Arg	Leu	Lys	Thr	Val	Ala	Thr
			340					345					350		
Ala	Val	Phe	Thr	Arg	Pro	Glu	Ile	Ala	Ala	Val	Gly	Ile	Thr	His	Ala
	355						360					365			
Gln	Val	Asp	Ser	Gly	Glu	Val	Ser	Ala	Arg	Val	Ile	Val	Leu	Pro	Leu
	370					375					380				
Ala	Thr	Asn	Pro	Arg	Ala	Lys	Met	Arg	Ser	Leu	Arg	His	Gly	Phe	Val
385					390					395					400
Lys	Leu	Phe	Cys	Arg	Arg	Asn	Ser	Gly	Leu	Ile	Ile	Gly	Gly	Val	Val
				405					410					415	
Val	Ala	Pro	Thr	Ala	Ser	Glu	Leu	Ile	Leu	Pro	Ile	Ala	Val	Ala	Val
			420					425					430		

Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr
 435 440 445

Pro Ser Leu Ser Gly Ser Ile Thr Glu Ala Ala Arg Gln Leu Val Gln
 450 455 460

His Asp Asp Leu Gly
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<210> 109

<211> 2895

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2872)

<223> RXA02259

<400> 109

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 Val Phe Lys Val Val
 1 5

atg act gat ttt tta cgc gat gac atc agg ttc ctc ggt caa atc ctc 163
 Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu
 10 15 20

ggt gag gta att gcg gaa caa gaa ggc cag gag gtt tat gaa ctg gtc 211
 Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val
 25 30 35

gaa caa gcg cgc ctg act tct ttt gat atc gcc aag ggc aac gcc gaa 259
 Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu
 40 45 50

atg gat agc ctg gtt cag gtt ttc gac ggc att act cca gcc aag gca 307
 Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala
 55 60 65

aca ccg att gct cgc gca ttt tcc cac ttc gct ctg ctg gct aac ctg 355
 Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu
 70 75 80 85

gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca 403
 Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala
 90 95 100

ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc 451
 Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu
 105 110 115

aat gag ggc aat gtt ggc gca gaa gct gtg gcc gat gtg ctg cgc aat 499
 Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn
 120 125 130

gct gag gtg gcg ccg gtt ctg act gcg cac cca act gag act cgc cgc 547

Ala	Glu	Val	Ala	Pro	Val	Leu	Thr	Ala	His	Pro	Thr	Glu	Thr	Arg	Arg		
135						140					145						
cgc	act	gtt	ttt	gat	gcg	caa	aag	tgg	atc	acc	acc	cac	atg	cgt	gaa	595	
Arg	Thr	Val	Phe	Asp	Ala	Gln	Lys	Trp	Ile	Thr	Thr	His	Met	Arg	Glu		
150					155				160					165			
cgc	cac	gct	ttg	cag	tct	gcg	gag	cct	acc	gct	cgt	acg	caa	agc	aag	643	
Arg	His	Ala	Leu	Gln	Ser	Ala	Glu	Pro	Thr	Ala	Arg	Thr	Gln	Ser	Lys		
				170					175					180			
ttg	gat	gag	atc	gag	aag	aac	atc	cgc	cgt	cgc	atc	acc	att	ttg	tgg	691	
Leu	Asp	Glu	Ile	Glu	Lys	Asn	Ile	Arg	Arg	Arg	Ile	Thr	Ile	Leu	Trp		
			185					190					195				
cag	acc	gcg	ttg	att	cgt	gtg	gcc	cgc	cda	cgt	atc	gag	gac	gag	atc	739	
Gln	Thr	Ala	Leu	Ile	Arg	Val	Ala	Arg	Pro	Arg	Ile	Glu	Asp	Glu	Ile		
	200					205						210					
gaa	gta	ggg	ctg	cgc	tac	tac	aag	ctg	agc	ctt	ttg	gaa	gag	att	cca	787	
Glu	Val	Gly	Leu	Arg	Tyr	Tyr	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Ile	Pro		
	215					220					225						
cgt	atc	aac	cgt	gat	gtg	gct	gtt	gag	ctt	cgt	gag	cgt	ttc	ggc	gag	835	
Arg	Ile	Asn	Arg	Asp	Val	Ala	Val	Glu	Leu	Arg	Glu	Arg	Phe	Gly	Glu		
230					235				240					245			
ggt	gtt	cct	ttg	aag	ccc	gtg	gtc	aag	cca	ggt	tcc	tgg	att	ggt	gga	883	
Gly	Val	Pro	Leu	Lys	Pro	Val	Val	Lys	Pro	Gly	Ser	Trp	Ile	Gly	Gly		
			250					255						260			
gac	cac	gac	ggt	aac	cct	tat	gtc	acc	gcg	gaa	aca	gtt	gag	tat	tcc	931	
Asp	His	Asp	Gly	Asn	Pro	Tyr	Val	Thr	Ala	Glu	Thr	Val	Glu	Tyr	Ser		
			265					270					275				
act	cac	cgc	gct	gcg	gaa	acc	gtg	ctc	aag	tac	tat	gca	cgc	cag	ctg	979	
Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	Tyr	Ala	Arg	Gln	Leu		
		280					285					290					
cat	tcc	ctc	gag	cat	gag	ctc	agc	ctg	tcg	gac	cgc	atg	aat	aag	gtc	1027	
His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp	Arg	Met	Asn	Lys	Val		
	295					300					305						
acc	ccg	cag	ctg	ctt	gcg	ctg	gca	gat	gca	ggg	cac	aac	gac	gtg	cca	1075	
Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly	His	Asn	Asp	Val	Pro		
310					315				320					325			
agc	cgc	gtg	gat	gag	cct	tat	cga	cgc	gcc	gtc	cat	ggc	gtt	cgc	gga	1123	
Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	His	Gly	Val	Arg	Gly		
				330				335						340			
cgt	atc	ctc	gcg	acg	acg	gcc	gag	ctg	atc	ggc	gag	gac	gcc	gtt	gag	1171	
Arg	Ile	Leu	Ala	Thr	Thr	Ala	Glu	Leu	Ile	Gly	Glu	Asp	Ala	Val	Glu		
			345				350						355				
ggc	gtg	tgg	ttc	aag	gtc	ttt	act	cca	tac	gca	tct	ccg	gaa	gaa	ttc	1219	
Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala	Ser	Pro	Glu	Glu	Phe		
	360						365					370					
tta	aac	gat	gcg	ttg	acc	att	gat	cat	tct	ctg	cgt	gaa	tcc	aag	gac	1267	
Leu	Asn	Asp	Ala	Leu	Thr	Ile	Asp	His	Ser	Leu	Arg	Glu	Ser	Lys	Asp		

375	380	385	
gtt ctc att gcc gat gat cgt ttg tct gtg ctg att tct gcc atc gag Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu Ile Ser Ala Ile Glu 390 395 400 405			1315
agc ttt gga ttc aac ctt tac gca ctg gat ctg cgc caa aac tcc gaa Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu Arg Gln Asn Ser Glu 410 415 420			1363
agc tac gag gac gtc ctc acc gag ctt ttc gaa cgc gcc caa gtc acc Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu Arg Ala Gln Val Thr 425 430 435			1411
gca aac tac cgc gag ctg tct gaa gca gag aag ctt gag gtg ctg ctg Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys Leu Glu Val Leu Leu 440 445 450			1459
aag gaa ctg cgc agc cct cgt ccg ctg atc ccg cac ggt tca gat gaa Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro His Gly Ser Asp Glu 455 460 465			1507
tac agc gag gtc acc gac cgc gag ctc ggc atc ttc cgc acc gcg tcg Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile Phe Arg Thr Ala Ser 470 475 480 485			1555
gag gct gtt aag aaa ttc ggg cca cgg atg gtg cct cac tgc atc atc Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val Pro His Cys Ile Ile 490 495 500			1603
tcc atg gca tca tcg gtc acc gat gtg ctc gag ccg atg gtg ttg ctc Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu Pro Met Val Leu Leu 505 510 515			1651
aag gaa ttc gga ctc atc gca gcc aac ggc gac aac cca cgc ggc acc Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp Asn Pro Arg Gly Thr 520 525 530			1699
gtc gat gtc atc cca ctg ttc gaa acc atc gaa gat ctc cag gcc ggc Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu Asp Leu Gln Ala Gly 535 540 545			1747
gcc gga atc ctc gac gaa ctg tgg aaa att gat ctc tac cgc aac tac Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp Leu Tyr Arg Asn Tyr 550 555 560 565			1795
ctc ctg cag cgc gac aac gtc cag gaa gtc atg ctc ggt tac tcc gat Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp 570 575 580			1843
tcc aac aag gat ggc gga tat ttc tcc gca aac tgg gcg ctt tac gac Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn Trp Ala Leu Tyr Asp 585 590 595			1891
gcg gaa ctg cag ctc gtc gaa cta tgc cga tca gcc ggg gtc aag ctt Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu 600 605 610			1939
cgc ctg ttc cac ggc cgt ggt ggc acc gtc ggc cgc ggt ggc gga cct Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro 615 620 625			1987

tcc tac gac gcg att ctt gcc cag ccc agg ggg gct gtc caa ggt tcc	2035
Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser	
630 635 640 645	
gtg cgc atc acc gag cag ggc gag atc atc tcc gct aag tac ggc aac	2083
Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn	
650 655 660	
ccc gaa acc gcg cgc cga aac ctc gaa gcc ctg gtc tca gcc acg ctt	2131
Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu	
665 670 675	
gag gca tcg ctt ctc gac gtc tcc gaa ctc acc gat cac caa cgc gcg	2179
Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala	
680 685 690	
tac gac atc atg agt gag atc tct gag ctc agc ttg aag aag tac gcc	2227
Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala	
695 700 705	
tcc ttg gtg cac gag gat caa ggc ttc atc gat tac ttc acc cag tcc	2275
Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser	
710 715 720 725	
acg ccg ctg cag gag att gga tcc ctc aac atc gga tcc agg cct tcc	2323
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser	
730 735 740	
tca cgc aag cag acc tcc tcg gtg gaa gat ttg cga gcc atc cca tgg	2371
Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp	
745 750 755	
gtg ctc agc tgg tca cag tct cgt gtc atg ctg cca ggc tgg ttt ggt	2419
Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly	
760 765 770	
gtc gga acc gca tta gag cag tgg att ggc gaa ggg gag cag gcc acc	2467
Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr	
775 780 785	
caa cgc att gcc gag ctg caa aca ctc aat gag tcc tgg cca ttt ttc	2515
Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe	
790 795 800 805	
acc tca gtg ttg gat aac atg gct cag gtg atg tcc aag gca gag ctg	2563
Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu	
810 815 820	
cgt ttg gca aag ctc tac gca gac ctg atc cca gat acg gaa gta gcc	2611
Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala	
825 830 835	
gag cga gtc tat tcc gtc atc cgc gag gag tac ttc ctg acc aag aag	2659
Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys	
840 845 850	
atg ttc tgc gta atc acc ggc tct gat gat ctg ctt gat gac aac cca	2707
Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro	
855 860 865	

ctt ctc gca cgc tct gtc cag cgc cga tac ccc tac ctg ctt cca ctc 2755
 Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro Tyr Leu Leu Pro Leu
 870 875 880 885

 aac gtg atc cag gta gag atg atg cga cgc tac cga aaa ggc gac caa 2803
 Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln
 890 895 900

 agc gag caa gtg tcc cgc aac att cag ctg acc atg aac ggt ctt tcc 2851
 Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser
 905 910 915

 act gcg ctg cgc aac tcc ggc tagtccagcc ggctgggtag tac 2895
 Thr Ala Leu Arg Asn Ser Gly
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<210> 110

<211> 924

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 110

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 Leu Gly Gln Ile Leu Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu
 20 25 30

 Val Tyr Glu Leu Val Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala
 35 40 45

 Lys Gly Asn Ala Glu Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile
 50 55 60

 Thr Pro Ala Lys Ala Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala
 65 70 75 80

 Leu Leu Ala Asn Leu Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu
 85 90 95

 Gln Ala Leu Asp Ala Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala
 100 105 110

 Thr Trp Leu Lys Leu Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala
 115 120 125

 Asp Val Leu Arg Asn Ala Glu Val Ala Pro Val Leu Thr Ala His Pro
 130 135 140

 Thr Glu Thr Arg Arg Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr
 145 150 155 160

 Thr His Met Arg Glu Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala
 165 170 175

 Arg Thr Gln Ser Lys Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg
 180 185 190

 Ile Thr Ile Leu Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg
 195 200 205

Ile Glu Asp Glu Ile Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu
 210 215 220
 Leu Glu Glu Ile Pro Arg Ile Asn Arg Asp Val Ala Val Glu Leu Arg
 225 230 235 240
 Glu Arg Phe Gly Glu Gly Val Pro Leu Lys Pro Val Val Lys Pro Gly
 245 250 255
 Ser Trp Ile Gly Gly Asp His Asp Gly Asn Pro Tyr Val Thr Ala Glu
 260 265 270
 Thr Val Glu Tyr Ser Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr
 275 280 285
 Tyr Ala Arg Gln Leu His Ser Leu Glu His Glu Leu Ser Leu Ser Asp
 290 295 300
 Arg Met Asn Lys Val Thr Pro Gln Leu Leu Ala Leu Ala Asp Ala Gly
 305 310 315 320
 His Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val
 325 330 335
 His Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly
 340 345 350
 Glu Asp Ala Val Glu Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala
 355 360 365
 Ser Pro Glu Glu Phe Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu
 370 375 380
 Arg Glu Ser Lys Asp Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu
 385 390 395 400
 Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu
 405 410 415
 Arg Gln Asn Ser Glu Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu
 420 425 430
 Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys
 435 440 445
 Leu Glu Val Leu Leu Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro
 450 455 460
 His Gly Ser Asp Glu Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile
 465 470 475 480
 Phe Arg Thr Ala Ser Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val
 485 490 495
 Pro His Cys Ile Ile Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu
 500 505 510
 Pro Met Val Leu Leu Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp
 515 520 525

Asn Pro Arg Gly Thr Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu
 530 535 540
 Asp Leu Gln Ala Gly Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp
 545 550 555 560
 Leu Tyr Arg Asn Tyr Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met
 565 570 575
 Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn
 580 585 590
 Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser
 595 600 605
 Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly
 610 615 620
 Arg Gly Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly
 625 630 635 640
 Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser
 645 650 655
 Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu
 660 665 670
 Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr
 675 680 685
 Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser
 690 695 700
 Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp
 705 710 715 720
 Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile
 725 730 735
 Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu
 740 745 750
 Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu
 755 760 765
 Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu
 770 775 780
 Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu
 785 790 795 800
 Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met
 805 810 815
 Ser Lys Ala Glu Leu Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro
 820 825 830
 Asp Thr Glu Val Ala Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr
 835 840 845
 Phe Leu Thr Lys Lys Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu

cgt cgc cgc ttc ggc aac acc tct gcg ctg gat gat cgt gaa ttc ttc 499

Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe
 120 125 130
 tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg 547
 Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val
 135 140 145
 cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat 595
 Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp
 150 155 160 165
 aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca 643
 Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro
 170 175 180
 atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa 691
 Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu
 185 190 195
 aag gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt 739
 Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
 200 205 210
 gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat 787
 Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp
 215 220 225
 gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct 835
 Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala
 230 235 240 245
 tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag 883
 Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys
 250 255 260
 gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270
 ccc 939

<210> 112

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
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Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
 20 25 30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr

65	70	75	80
Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys	85	90	95
Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu	100	105	110
Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp	115	120	125
Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile	130	135	140
Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile	145	150	155
Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn	165	170	175
Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val	180	185	190
Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala	195	200	205
Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu	210	215	220
Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu	225	230	235
Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val	245	250	255
Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser	260	265	270

<210> 113

<211> 939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(916)

<223> FRXA02326

<400> 113

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Met Leu Gly Arg Pro	
1 5	

acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac	163
Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His	

10							15							20							
ctc	ggt	ggt	gcg	ggt	gtg	gat	cca	gca	gac	ttt	gct	gcc	gat	cca	caa	211					
Leu	Val	Gly	Ala	Gly	Val	Asp	Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln						
			25					30					35								
aag	tac	gac	atc	cca	gac	tct	gtc	atc	gcg	ttc	ctg	cgc	ggc	gag	ctt	259					
Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu						
			40					45					50								
ggt	aac	cct	cca	ggt	ggc	tgg	cca	gag	cca	ctg	cgc	acc	cgc	gca	ctg	307					
Gly	Asn	Pro	Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu						
			55					60					65								
gaa	ggc	cgc	tcc	gaa	ggc	aag	gca	cct	ctg	acg	gaa	gtt	cct	gag	gaa	355					
Glu	Gly	Arg	Ser	Glu	Gly	Lys	Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu						
			70					75					80		85						
gag	cag	gcg	cac	ctc	gac	gct	gat	gat	tcc	aag	gaa	cgt	cgc	aat	agc	403					
Glu	Gln	Ala	His	Leu	Asp	Ala	Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser						
			90					95					100								
ctc	aac	cgc	ctg	ctg	ttc	ccg	aag	cca	acc	gaa	gag	ttc	ctc	gag	cac	451					
Leu	Asn	Arg	Leu	Leu	Phe	Pro	Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His						
			105					110					115								
cgt	cgc	cgc	ttc	ggc	aac	acc	tct	gcg	ctg	gat	gat	cgt	gaa	ttc	ttc	499					
Arg	Arg	Arg	Phe	Gly	Asn	Thr	Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe						
			120					125					130								
tac	ggc	ctg	gtc	gaa	ggc	cgc	gag	act	ttg	atc	cgc	ctg	cca	gat	gtg	547					
Tyr	Gly	Leu	Val	Glu	Gly	Arg	Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val						
			135					140					145								
cgc	acc	cca	ctg	ctt	gtt	cgc	ctg	gat	gcg	atc	tct	gag	cca	gac	gat	595					
Arg	Thr	Pro	Leu	Leu	Val	Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp						
150						155					160					165					
aag	ggt	atg	cgc	aat	gtt	gtg	gcc	aac	gtc	aac	ggc	cag	atc	cgc	cca	643					
Lys	Gly	Met	Arg	Asn	Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro						
			170					175					180								
atg	cgt	gtg	cgt	gac	cgc	tcc	gtt	gag	tct	gtc	acc	gca	acc	gca	gaa	691					
Met	Arg	Val	Arg	Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu						
			185					190					195								
aag	gca	gat	tcc	tcc	aac	aag	ggc	cat	gtt	gct	gca	cca	ttc	gct	ggt	739					
Lys	Ala	Asp	Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly						
			200					205					210								
gtt	gtc	acc	gtg	act	gtt	gct	gaa	ggt	gat	gag	gtc	aag	gct	gga	gat	787					
Val	Val	Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp						
			215					220					225								
gca	gtc	gca	atc	atc	gag	gct	atg	aag	atg	gaa	gca	aca	atc	act	gct	835					
Ala	Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala						
230						235					240					245					
tct	gtt	gac	ggc	aaa	atc	gat	cgc	gtt	gtg	gtt	cct	gct	gca	acg	aag	883					
Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr	Lys						
			250					255					260								

gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270

ccc

939

<210> 114

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
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Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
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Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65 70 75 80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
 85 90 95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
 100 105 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
 115 120 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 130 135 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 145 150 155 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
 165 170 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
 180 185 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
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Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
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 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
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 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
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 Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
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 Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
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 Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
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 Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
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Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
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Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
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Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
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Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
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 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
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 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
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 Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
 115 120 125
 Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
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 Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160
 His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175
 Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190
 His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
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 Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
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 Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240
 Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
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 Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
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Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
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Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
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Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
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Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
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Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
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Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
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acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
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 Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
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 Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
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 Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
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Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
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Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
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Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
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Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
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Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
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Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
 130 135 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
 195 200 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
 210 215 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
 245 250 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
 260 265 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
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 Val Thr Ala Ile Thr
 1 5
 ctt ggc ggt ctc ttg ttg aaa gga ata att act cta gtg tcg act cac 163

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Gly	Glu	Ile	Ala	Val	Arg	Ala	Phe	Arg	Ala	Ala	Leu	Glu	Thr	Gly	Ala		
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Ala	Thr	Val	Ala	Ile	Tyr	Pro	Arg	Glu	Asp	Arg	Gly	Ser	Phe	His	Arg		
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Ser	Phe	Ala	Ser	Glu	Ala	Val	Arg	Ile	Gly	Thr	Glu	Gly	Ser	Pro	Val		
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Lys	Ala	Asp	Ala	Ile	Tyr	Pro	Gly	Tyr	Gly	Phe	Leu	Ser	Glu	Asn	Ala		
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Gln	Leu	Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr	Phe	Ile	Gly	Pro		
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Thr	Pro	Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser	Arg	Ala	Val	Thr		
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Ala	Ala	Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu	Ser	Thr	Pro	Ser		
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Ile	Phe	Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Phe		
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His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu															
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Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg															
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470					475				480					485																
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cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc 1696
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<213> Corynebacterium glutamicum

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Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
 65 70 75 80

Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
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Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
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Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
 115 120 125

Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys
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Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala
 145 150 155 160

Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu
 165 170 175

Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly
 180 185 190

Arg Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala
 195 200 205

Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val
 210 215 220

Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile

225 230 235 240
 Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys
 245 250 255
 Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln
 260 265 270
 His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys
 275 280 285
 Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu
 290 295 300
 Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile
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 Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val
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 Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly
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 Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg
 355 360 365
 Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr
 370 375 380
 Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly
 385 390 395 400
 Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu
 405 410 415
 Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg
 420 425 430
 Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn
 435 440 445
 Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys
 450 455 460
 Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala
 465 470 475 480
 Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp
 485 490 495
 Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala
 500 505 510
 Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly
 515 520 525
 Ser Arg Asp Arg
 530

<210> 121

<211> 1406
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1383)
 <223> FRXA02328

<400> 121

gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc aag gcg	48
Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala	
1 5 10 15	
tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt aaa gca	96
Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala	
20 25 30	
gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc cag ctt	144
Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu	
35 40 45	
gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca acc cca	192
Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro	
50 55 60	
gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc gcc gcg	240
Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala	
65 70 75 80	
aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc aaa aac	288
Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn	
85 90 95	
atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc atc ttt	336
Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe	
100 105 110	
gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt gtt gct	384
Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala	
115 120 125	
tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt gaa gct	432
Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala	
130 135 140	
gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct gtg att	480
Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile	
145 150 155 160	
aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act gga gaa	528
Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu	
165 170 175	
gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt cac caa	576
Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln	
180 185 190	
aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa ctg cgt	624
Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg	
195 200 205	

gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att ggt tac	672
Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr	
210 215 220	
cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc aac cac	720
Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His	
225 230 235 240	
gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc gtg act	768
Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr	
245 250 255	
gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc ttg gct	816
Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala	
260 265 270	
gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag atc aag	864
Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys	
275 280 285	
acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat cca aac	912
Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn	
290 295 300	
aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc tca cca	960
Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro	
305 310 315 320	
ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt ggc gaa	1008
Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu	
325 330 335	
atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc cgt ggt	1056
Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly	
340 345 350	
tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg gct gag	1104
Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu	
355 360 365	
ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt gcg ttg	1152
Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu	
370 375 380	
ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga ttc att	1200
Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile	
385 390 395 400	
gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat gag cag	1248
Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln	
405 410 415	
gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag cct cat	1296
Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His	
420 425 430	
ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg cct aac	1344
Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn	
435 440 445	

atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc tgaagcagct 1393
 ile lys asp leu pro leu pro arg gly ser arg asp arg
 450 455 460

tggcccagcc gcg 1406

<210> 122

<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
 1 5 10 15

Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
 20 25 30

Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
 35 40 45

Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
 50 55 60

Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala
 65 70 75 80

Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn
 85 90 95

Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
 100 105 110

Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
 115 120 125

Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
 130 135 140

Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
 145 150 155 160

Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
 165 170 175

Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
 180 185 190

Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg
 195 200 205

Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr
 210 215 220

Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His
 225 230 235 240

Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr
 245 250 255

Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala
 260 265 270
 Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys
 275 280 285
 Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn
 290 295 300
 Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro
 305 310 315 320
 Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu
 325 330 335
 Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly
 340 345 350
 Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu
 355 360 365
 Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu
 370 375 380
 Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
 385 390 395 400
 Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
 405 410 415
 Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
 420 425 430
 Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
 435 440 445
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

<210> 123

<211> 1347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1324)

<223> RXN01048

<400> 123

agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60
 gagcttcccc caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly	
250 255 260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931

Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405

cca ata ttt taagagcaaa cttgaggccc aca 1347
 Pro Ile Phe

<210> 124

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile
 305 310 315 320
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala
 325 330 335
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln
 340 345 350
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu
 355 360 365
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg
 370 375 380
 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
 385 390 395 400
 Leu Pro Val Glu Ala Pro Ile Phe

405

<210> 125
 <211> 311
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(288)
 <223> FRXA01048

<400> 125
 cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga 48
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15
 att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80
 aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
 85 90 95
 taagagcaaa cttgaggccc aca 311

<210> 126
 <211> 96
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 126
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80

tct ttc ggt gct atc aac' ttg gag gac atc tcc gct cct cgt tgc ttc 547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
135 140 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
 Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
 150 155 160 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
 Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
 170 175 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
 Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
 185 190 195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac 739
 Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
 200 205 210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac 787
 Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
 215 220 225

gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag 835
 Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
 230 235 240 245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
 250 255 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
 310 315 320

<210> 128

<211> 321

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 128

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr

50	55	60
His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala 65 70 75 80		
Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met 85 90 95		
Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile 100 105 110		
Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile 115 120 125		
Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser 130 135 140		
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 145 150 155 160		
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 175		
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp 180 185 190		
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205		
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220		
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240		
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255		
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270		
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285		
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 290 295 300		
Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg 305 310 315 320		
Ser		

<210> 129

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA02694

<400> 129

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tgggttgtcc ggtagggaa atcaggaagt gggatcgaaa atg aaa gaa acc gtc 115
 Met Lys Glu Thr Val
 1 5

ggt aac aag att gtc ctc att ggc gca gga gat gtt gga gtt gca tac 163
 Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp Val Gly Val Ala Tyr
 10 15 20

gca tac gca ctg atc aac cag ggc atg gca gat cac ctt gcg atc atc 211
 Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp His Leu Ala Ile Ile
 25 30 35

gac atc gat gaa aag aaa ctc gaa ggc aac gtc atg gac tta aac cat 259
 Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val Met Asp Leu Asn His
 40 45 50

ggt gtt gtg tgg gcc gat tcc cgc acc cgc gtc acc aag ggc acc tac 307
 Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val Thr Lys Gly Thr Tyr
 55 60 65

gct gac tgc gaa gac gca gcc atg gtt gtc att tgt gcc ggc gca gcc 355
 Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile Cys Ala Gly Ala Ala
 70 75 80 85

caa aag cca ggc gag acc cgc ctc cag ctg gtg gac aaa aac gtc aag 403
 Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val Asp Lys Asn Val Lys
 90 95 100

att atg aaa tcc atc gtc ggc gat gtc atg gac agc gga ttc gac ggc 451
 Ile Met Lys Ser Ile Val Gly Asp Val Met Asp Ser Gly Phe Asp Gly
 105 110 115

atc ttc ctc gtg gcg tcc aac cca gtg gat atc ctg acc tac gca gtg 499
 Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile Leu Thr Tyr Ala Val
 120 125 130

tgg aaa ttc tcc ggc ttg gaa tgg aac cgc gtg atc ggc tcc gga act 547
 Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val Ile Gly Ser Gly Thr
 135 140 145

gtc ctg gac tcc gct cga ttc cgc tac atg ctg ggc gaa ctc tac gaa 595
 Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu Gly Glu Leu Tyr Glu
 150 155 160 165

gtg gca cca agc tcc gtc cac gcc tac atc atc ggc gaa cac ggc gac 643
 Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile Gly Glu His Gly Asp
 170 175 180

act gaa ctt cca gtc ctg tcc tcc gcg acc atc gca ggc gta tcg ctt 691
 Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile Ala Gly Val Ser Leu
 185 190 195

agc cga atg ctg gac aaa gac cca gag ctt gag ggc cgt cta gag aaa 739
 Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys
 200 205 210

att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag 787
 Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys
 215 220 225

 ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc 835
 Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg
 230 235 240 245

 gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc 883
 Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu
 250 255 260

 cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg 931
 His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val
 265 270 275

 gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac 979
 Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp
 280 285 290

 cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att 1027
 His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile
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 Gln Lys Gln Phe Phe
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<210> 130

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<212> PRT

<213> Corynebacterium glutamicum

<400> 130

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 20 25 30

 His Leu Ala Ile Ile Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val
 35 40 45

 Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val
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 Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile
 65 70 75 80

 Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val
 85 90 95

 Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp
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 Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile
 115 120 125

 Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val

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<222> (101)..(2944)
<223> RXN00296
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                                         Met Thr His Thr Ile
                                         . 1                               5

aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct cgc gcg 163
Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser Arg Ala
                        10                        15                        20

aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct gat gca 211
Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser Asp Ala
                        25                        30                        35

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gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa aat gtg	259
Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu Asn Val	
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gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg tgg tct	307
Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly Trp Ser	
55 60 65	
gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg atc ggt	355
Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala Ile Gly	
70 75 80 85	
gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att tta gat	403
Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile Leu Asp	
90 95 100	
att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg gtg tgt	451
Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val Val Cys	
105 110 115	
gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac ggc ccg	499
Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr Gly Pro	
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gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt gcc aac	547
Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val Ala Asn	
135 140 145	
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Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala Glu Asn	
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Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val Thr Val	
170 175 180	
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Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu Thr Asp	
185 190 195	
tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt cgt ttc	739
Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly Arg Phe	
200 205 210	
cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac gac atg	787
Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His Asp Met	
215 220 225	
gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att act cgg	835
Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile Thr Arg	
230 235 240 245	
ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt gct gtc	883
Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu Ala Val	
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ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc aaa ttg	931
Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala Lys Leu	
265 270 275	
cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat ctc ctc	979

Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp	Leu	Leu	
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gct	gcg	ctg	cgc	agt	aaa	cag	gga	caa	tca	gaa	gct	ggg	cag	aat	ctt	1027
Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	Ala	Gly	Gln	Asn	Leu	
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cca	gga	aac	cgc	atc	ggc	att	gaa	gcc	ggc	gga	tgg	ttg	tac	tgc	gag	1075
Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly	Trp	Leu	Tyr	Cys	Glu	
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aca	gga	agt	gac	acc	ctg	cag	gcc	gcg	gta	caa	gcc	gcc	gag	gaa	gtc	1123
Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu	Glu	Val	
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gca	acc	gcc	gtt	gac	acc	att	gat	tac	gtg	gtc	gtg	tct	gag	cct	tct	1171
Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val	Val	Ser	Glu	Pro	Ser	
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Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	Ser	Ala	Gly	Ile	Val	
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Thr	Arg	Leu	Ala	Asp	Gly	Glu	Glu	Ala	Trp	Pro	Asn	Trp	Glu	Asp	Ser	
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gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	tat	gcg	1315
Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	Tyr	Ala	
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ctg	atg	gat	aag	ttc	gat	tac	cag	ggg	att	cca	ttt	gga	cac	ttt	gga	1363
Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	Phe	Gly	
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gaa	ggc	tgc	gtc	cac	gtt	cgc	atc	agt	ttt	gat	ttc	tct	acc	aag	gaa	1411
Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	Lys	Glu	
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Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	Leu	Val	
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gcg	tct	tat	ggg	ggc	agc	ctc	tcg	ggc	gag	cat	gga	gac	ggg	cgc	gcc	1507
Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	Arg	Ala	
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cgc	tca	tcc	ttc	ctt	gac	cgc	atg	tat	tca	gca	gaa	atg	cgt	gca	ctc	1555
Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala	Glu	Met	Arg	Ala	Leu	
470					475					480					485	
ttc	gaa	gaa	ttc	aag	ctg	att	ttc	gat	ccc	cag	cgc	atc	ttc	aat	ccg	1603
Phe	Glu	Glu	Phe	Lys	Leu	Ile	Phe	Asp	Pro	Gln	Arg	Ile	Phe	Asn	Pro	
				490					495					500		
gga	gtg	ttg	gtc	tgg	gca	gat	cct	gtc	atg	caa	gga	ctt	cgc	atg	gac	1651
Gly	Val	Leu	Val	Trp	Ala	Asp	Pro	Val	Met	Gln	Gly	Leu	Arg	Met	Asp	
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ccg	ggc	cag	cgc	gcc	ctc	gac	atc	acg	ccc	gta	cac	aaa	ttc	tct	aaa	1699
Pro	Gly	Gln	Arg	Ala	Leu	Asp	Ile	Thr	Pro	Val	His	Lys	Phe	Ser	Lys	

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tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt ctt cct Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu Leu Pro 650 655 660			2083
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cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc gcc cac Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe Ala His 680 685 690			2179
cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa acg gtg Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu Thr Val 695 700 705			2227
gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga cca gct Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly Pro Ala 710 715 720 725			2275
cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg gtc atc His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val Val Ile 730 735 740			2323
cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc ggc caa Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr Gly Gln 745 750 755			2371
ttg agc atg aca aag aaa gtc cta gaa caa acg gcg aaa gtg atg aaa Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val Met Lys 760 765 770			2419

ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct tcg tgc 2467
 Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys
 775 780 785

acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac cct gat 2515
 Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn Pro Asp
 790 795 800 805

ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc atc gca 2563
 Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val Ile Ala
 810 815 820

cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta aca gaa 2611
 Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu Thr Glu
 825 830 835

tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta ggc gac 2659
 Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu Gly Asp
 840 845 850

cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa gat gaa 2707
 Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys Asp Glu
 855 860 865

caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc ttt gaa 2755
 Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly Phe Glu
 870 875 880 885

aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag ctg ttc 2803
 Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu Leu Phe
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 Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly Phe Ser
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 Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr His Leu
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gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca caa 2944
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Gly	Asn	Ala	Ile	Gly	Glu	Gly	Leu	Ile	Ile	Asp	Thr	Ser	Arg	Tyr	Phe
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Asn	Arg	Ile	Leu	Asp	Ile	Asp	Pro	Val	Ala	Gln	Thr	Ala	Val	Val	Glu
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Pro	Gly	Val	Val	Cys	Asp	Ala	Leu	Arg	Asp	Ala	Ala	Ala	Glu	Phe	Gly
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Leu	Thr	Tyr	Gly	Pro	Asp	Pro	Ser	Thr	His	Ser	Arg	Cys	Thr	Ile	Gly
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Gly	Met	Val	Ala	Asn	Asn	Ala	Cys	Gly	Ser	His	Ser	Val	Ala	Phe	Gly
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Thr	Ala	Ala	Glu	Asn	Leu	Val	Asp	Val	Thr	Leu	Met	Leu	Ser	Asp	Gly
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Arg	Glu	Val	Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn
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Gln	Lys	Leu	Thr	Asp	Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys
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Leu	Ala	His	Asp	Met	Ala	Lys	Ala	Met	Ala	Gly	Thr	Glu	Gly	Thr	Ile
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Gly	Ile	Ile	Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val
				245					250					255	
Lys	Ala	Leu	Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg
			260					265					270		
Ala	Ala	Ala	Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met
			275				280					285			
Gly	Gly	Asp	Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu
			290			295					300				
Ala	Gly	Gln	Asn	Leu	Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly
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Trp	Leu	Tyr	Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln
				325					330					335	
Ala	Ala	Glu	Glu	Val	Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val
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Val	Ser	Glu	Pro	Ser	Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser
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Ser Ala Gly Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro
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 Asn Trp Glu Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu
 385 390 395 400
 Arg Asp Leu Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro
 405 410 415
 Phe Gly His Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp
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 Phe Ser Thr Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu
 435 440 445
 Ala Ser Thr Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His
 450 455 460
 Gly Asp Gly Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala
 465 470 475 480
 Glu Met Arg Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln
 485 490 495
 Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln
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 Gly Leu Arg Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val
 515 520 525
 His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg
 530 535 540
 Cys Val Gly Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro
 545 550 555 560
 Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala
 565 570 575
 Arg Leu Leu Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr
 580 585 590
 Arg Ser Glu Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys
 595 600 605
 Ala Cys Ala Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys
 610 615 620
 Ala Glu Phe Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala
 625 630 635 640
 His Tyr Val Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys
 645 650 655
 Ile Pro Leu Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu
 660 665 670
 Thr Ala Pro Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu
 675 680 685

Ile Ser Phe Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn
 690 695 700
 Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu
 705 710 715 720
 Asp Thr Gly Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly
 725 730 735
 Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp
 740 745 750
 His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr
 755 760 765
 Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly
 770 775 780
 Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu
 785 790 795 800
 Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe
 805 810 815
 Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser
 820 825 830
 Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu
 835 840 845
 Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu
 850 855 860
 Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly
 865 870 875 880
 Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly
 885 890 895
 Glu Arg Glu Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile
 900 905 910
 Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys
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 Gln Ala Thr His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn
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<210> 133

<211> 2858

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (1)..(2835)

<223> FRXA00296

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Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser	
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Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu	
35 40 45	
aat gtg gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg	192
Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly	
50 55 60	
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Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala	
65 70 75 80	
atc ggt gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att	288
Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile	
85 90 95	
tta gat att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg	336
Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val	
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gtg tgt gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac	384
Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr	
115 120 125	
ggc ccg gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt	432
Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val	
130 135 140	
gcc aac aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg	480
Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala	
145 150 155 160	
gaa aat ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc	528
Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val	
165 170 175	
act gtg aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc	576
Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu	
180 185 190	
acc gac tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt	624
Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly	
195 200 205	
cgt ttc cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac	672
Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His	
210 215 220	
gac atg gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att	720
Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile	
225 230 235 240	

act cgg ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt	768
Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu	
245 250 255	
gct gtc ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc	816
Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala	
260 265 270	
aaa ttg cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat	864
Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp	
275 280 285	
ctc ctc gct gcg ctg cgc agt aaa cag gga caa tca gaa gct ggg cag	912
Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln	
290 295 300	
aat ctt cca gga aac cgc atc ggc att gaa gcc ggc gga tgg ttg tac	960
Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr	
305 310 315 320	
tgc gag aca gga agt gac acc ctg cag gcc gcg gta caa gcc gcc gag	1008
Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu	
325 330 335	
gaa gtc gca acc gcc gtt gac acc att gat tac gtg gtc gtg tct gag	1056
Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu	
340 345 350	
cct tct gaa atg cgg gaa ttg tgg cgc atc cgt gaa tcc tcg gcg ggc	1104
Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly	
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att gtc acg cgc tta gct gat ggt ggg gaa gcg tgg ccg aat tgg gaa	1152
Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu	
370 375 380	
gac tcg gcg gtg cct cca gag aat tta gct gat tat ctc cgc gat ctt	1200
Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu	
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tat gcg ctg atg gat aag ttc gat tac cag ggt att cca ttt gga cac	1248
Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His	
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Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr	
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aag gaa ggc ctg aag aaa ttc gag gcg ttc atg aat gaa gcc tcc acc	1344
Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr	
435 440 445	
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Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly	
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cgc gcc cgc tca tcc ttc ctt gac cgc atg tat tca gca gaa atg cgt	1440
Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg	
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Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe	
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Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg	
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Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe	
515 520 525	
tct aaa gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt	1632
Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly	
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gta tcc gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa	1680
Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln	
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Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu	
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Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu	
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Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala	
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tcg gaa tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc	1872
Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe	
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ctg gac aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc	1920
Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val	
625 630 635 640	
atg ggc tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt	1968
Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu	
645 650 655	
ctt cct acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca	2016
Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro	
660 665 670	
gtg gtg cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc	2064
Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe	
675 680 685	
gcc cac cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa	2112
Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu	
690 695 700	
acg gtg gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga	2160
Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly	
705 710 715 720	
cca gct cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg	2208

Pro	Ala	His	Ala	Ala	Ile	Lys	Thr	Leu	Glu	Ala	Leu	Gly	Tyr	Asn	Val	
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gtc	atc	cca	gat	ggc	ttc	gtc	tgc	tgt	gga	ctc	acc	tgg	cat	tcc	acc	2256
Val	Ile	Pro	Asp	Gly	Phe	Val	Cys	Cys	Gly	Leu	Thr	Trp	His	Ser	Thr	
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ggc	caa	ttg	agc	atg	aca	aag	aaa	gtc	cta	gaa	caa	acg	gcg	aaa	gtg	2304
Gly	Gln	Leu	Ser	Met	Thr	Lys	Lys	Val	Leu	Glu	Gln	Thr	Ala	Lys	Val	
			755					760					765			
atg	aaa	ccc	tac	ctg	gac	caa	ggt	cta	aca	gtc	gtt	ggt	ttg	gaa	cct	2352
Met	Lys	Pro	Tyr	Leu	Asp	Gln	Gly	Leu	Thr	Val	Val	Gly	Leu	Glu	Pro	
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Ser	Cys	Thr	Val	Met	Leu	Gln	Asp	Glu	Ala	Thr	Glu	Leu	Ser	Asp	Asn	
					790					795					800	
cct	gat	ctg	gca	cgc	ctt	gca	gca	ctg	acc	aaa	cca	ttc	gct	gag	gtc	2448
Pro	Asp	Leu	Ala	Arg	Leu	Ala	Ala	Leu	Thr	Lys	Pro	Phe	Ala	Glu	Val	
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atc	gca	cca	aag	atc	acc	gag	cta	gtc	gag	tct	gga	agc	ctc	cag	cta	2496
Ile	Ala	Pro	Lys	Ile	Thr	Glu	Leu	Val	Glu	Ser	Gly	Ser	Leu	Gln	Leu	
			820					825						830		
aca	gaa	tca	act	gcg	ctt	acc	cag	gtg	cac	tgc	cac	gag	cgt	tcg	cta	2544
Thr	Glu	Ser	Thr	Ala	Leu	Thr	Gln	Val	His	Cys	His	Glu	Arg	Ser	Leu	
			835					840					845			
ggc	gac	cca	caa	caa	tcg	gca	ctc	gtt	ctt	gaa	gct	ttg	ggt	gta	aaa	2592
Gly	Asp	Pro	Gln	Gln	Ser	Ala	Leu	Val	Leu	Glu	Ala	Leu	Gly	Val	Lys	
			850				855					860				
gat	gaa	caa	att	gcc	act	ggt	tgt	tgc	ggg	ctt	gcc	gga	aac	tgg	ggc	2640
Asp	Glu	Gln	Ile	Ala	Thr	Gly	Cys	Cys	Gly	Leu	Ala	Gly	Asn	Trp	Gly	
					870					875					880	
ttt	gaa	aaa	gac	cac	gct	gaa	atg	tcc	ttc	gca	ctt	ggt	gaa	cga	gag	2688
Phe	Glu	Lys	Asp	His	Ala	Glu	Met	Ser	Phe	Ala	Leu	Gly	Glu	Arg	Glu	
				885					890					895		
ctg	ttc	ccc	aag	gtc	aga	aaa	gca	gaa	gga	cat	gtg	att	gct	gac	ggt	2736
Leu	Phe	Pro	Lys	Val	Arg	Lys	Ala	Glu	Gly	His	Val	Ile	Ala	Asp	Gly	
			900					905						910		
ttc	tcc	tgc	cgc	acc	cag	atc	gaa	caa	ggc	acc	gga	aaa	caa	gca	acg	2784
Phe	Ser	Cys	Arg	Thr	Gln	Ile	Glu	Gln	Gly	Thr	Gly	Lys	Gln	Ala	Thr	
			915					920					925			
cac	ctt	gca	gag	gtg	gtc	tta	agc	atc	ttg	gag	caa	aac	aac	atg	gca	2832
His	Leu	Ala	Glu	Val	Val	Leu	Ser	Ile	Leu	Glu	Gln	Asn	Asn	Met	Ala	
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caa	taacgatcat	gcaacaggtg	ctc													2858
Gln																
945																

<210> 134

<211> 945

<212> PRT

<213> *Corynebacterium glutamicum*

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 Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu
 35 40 45
 Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly
 50 55 60
 Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala
 65 70 75 80
 Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile
 85 90 95
 Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val
 100 105 110
 Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr
 115 120 125
 Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val
 130 135 140
 Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala
 145 150 155 160
 Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val
 165 170 175
 Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu
 180 185 190
 Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly
 195 200 205
 Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His
 210 215 220
 Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile
 225 230 235 240
 Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu
 245 250 255
 Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala
 260 265 270
 Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp
 275 280 285
 Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln
 290 295 300

Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr
 305 310 315 320
 Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu
 325 330 335
 Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu
 340 345 350
 Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly
 355 360 365
 Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu
 370 375 380
 Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu
 385 390 395 400
 Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His
 405 410 415
 Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr
 420 425 430
 Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr
 435 440 445
 Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly
 450 455 460
 Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg
 465 470 475 480
 Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe
 485 490 495
 Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg
 500 505 510
 Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe
 515 520 525
 Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly
 530 535 540
 Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln
 545 550 555 560
 Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu
 565 570 575
 Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu
 580 585 590
 Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala
 595 600 605
 Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe
 610 615 620

Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val
 625 630 635 640
 Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu
 645 650 655
 Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro
 660 665 670
 Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe
 675 680 685
 Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu
 690 695 700
 Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly
 705 710 715 720
 Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val
 725 730 735
 Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr
 740 745 750
 Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val
 755 760 765
 Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro
 770 775 780
 Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn
 785 790 795 800
 Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val
 805 810 815
 Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu
 820 825 830
 Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu
 835 840 845
 Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys
 850 855 860
 Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly
 865 870 875 880
 Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu
 885 890 895
 Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly
 900 905 910
 Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr
 915 920 925
 His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala
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 Gln

945

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<223> RXA01901
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	Met Val Lys Arg Gln 1 5
ctg ccc aac ccc gca gaa cta ctg gaa ctg atg aag ttc aaa aag cca	163
Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met Lys Phe Lys Lys Pro	10 15 20
gag ctg aac gcc aag aaa cga cgc cta gag tcc gcg ctg acc atc tac	211
Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser Ala Leu Thr Ile Tyr	25 30 35
gac ctg cgt aaa att gct aaa cga cgc acc cca gct gcc gcg ttc gag	259
Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro Ala Ala Phe Asp	40 45 50
tac acc gag gcc gca gcc gag gcc gaa ctg tca atc acg cgc gca cgt	307
Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser Ile Thr Arg Ala Arg	55 60 65
gaa gca' ttc gaa aac atc gaa ttc cac cca gag atc ctg aag cct gca	355
Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp Ile Leu Lys Pro Ala	70 75 80 85
gaa cac gta gag acc acc acc caa atc ctg gcc gga acc tcc tcc atg	403
Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly Gly Thr Ser Ser Met	90 95 100
cca ttc gcc atc gca cca acc gcc ttc acc cgc ctg atg cag acc gaa	451
Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg Leu Met Gln Thr Glu	105 110 115
ggg gaa atc gca ggt gcc gga gct gca gcc gct gca gga att cct ttc	499
Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala Ala Gly Ile Pro Phe	120 125 130
acc ctg tcc acc ctg gcc act acc tcc atc gaa gag gtc aag gcc acc	547
Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu Asp Val Lys Ala Thr	135 140 145
aac ccc aac gcc cga aac tgg ttc cag ctg tac gtc atg cgc gag cgc	595
Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr Val Met Arg Asp Arg	150 155 160 165
gaa atc tcc tac gcc ctg gtc gaa cgc gca gcc aaa gca gga ttc gag	643

Glu Ile Ser Tyr	Gly Leu Val	Glu Arg	Ala Ala	Lys Ala	Gly Phe Asp	
	170		175		180	
acc ctg atg ttc acc gtg gat acc ccc atc gcc ggc tac cgc atc cgc						691
Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala Gly Tyr Arg Ile Arg	185	190		195		
gat tcc cgc aac gga ttc tcc atc ccg cca cag ctg acc cca tcc acc						739
Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln Leu Thr Pro Ser Thr	200	205		210		
gtg ctc aat gca atc cca cgc cca tgg tgg tgg atc gac ttc ctg acc						787
Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp Ile Asp Phe Leu Thr	215	220		225		
acc cca acc ctt gag ttc gca tcc ctt tcc tcg acc ggc gga acc gtg						835
Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Thr Gly Gly Thr Val	230	235		240	245	
ggc gac ctc ctc aac tcc gcg atg gat ccc acc att tct tac gaa gac						883
Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr Ile Ser Tyr Glu Asp	250	255		260		
ctc aag gtc atc cgt gaa atg tgg cca ggc aag ctc gta gtc aag ggt						931
Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys Leu Val Val Lys Gly	265	270		275		
gtc cag aac gtt gaa gac tcc gtc aaa ctc ctc gac caa ggc gtc gac						979
Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu Asp Gln Gly Val Asp	280	285		290		
ggc ctc atc ctc tcc aac cac ggt ggc cgt caa ctc gac cgc gca cca						1027
Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln Leu Asp Arg Ala Pro	295	300		305		
gtc cca ttc cac ctc ctg cca cag gta cgc aag gaa gtc gga tct gaa						1075
Val Pro Phe His Leu Leu Pro Gln Val Arg Lys Glu Val Gly Ser Glu	310	315		320	325	
cca acc atc atg atc gac acc ggc atc atg aac ggc gcc gac atc gtc						1123
Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn Gly Ala Asp Ile Val	330	335		340		
gca gcc gta gcc atg ggc gct gac ttc acc ctc atc ggt cgt gcc tac						1171
Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu Ile Gly Arg Ala Tyr	345	350		355		
ctc tac gga ctc atg gcc gga ggc cgc gaa ggc gtc gac cgc acc atc						1219
Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly Val Asp Arg Thr Ile	360	365		370		
gcc att ctc cgc agc gag atc acc cgc acc atg gct ctc ctc ggt gtt						1267
Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met Ala Leu Leu Gly Val	375	380		385		
tcc tcc ctc gaa gaa ctc gag cca cgc cac gtc acc cag ctg gcc aag						1315
Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val Thr Gln Leu Ala Lys	390	395		400	405	
atg gtt cca gtt tct gac gca act cgt tct gca gcg gcg gag att						1360
Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala Ala Ala Glu Ile						

410

415

420

taaaagtttc tctccttagc tat

1383

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<213> Corynebacterium glutamicum

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Ala Leu Thr Ile Tyr Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro
 35 40 45

Ala Ala Ala Phe Asp Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser
 50 55 60

Ile Thr Arg Ala Arg Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp
 65 70 75 80

Ile Leu Lys Pro Ala Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly
 85 90 95

Gly Thr Ser Ser Met Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg
 100 105 110

Leu Met Gln Thr Glu Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala
 115 120 125

Ala Gly Ile Pro Phe Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu
 130 135 140

Asp Val Lys Ala Thr Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr
 145 150 155 160

Val Met Arg Asp Arg Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala
 165 170 175

Lys Ala Gly Phe Asp Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala
 180 185 190

Gly Tyr Arg Ile Arg Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln
 195 200 205

Leu Thr Pro Ser Thr Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp
 210 215 220

Ile Asp Phe Leu Thr Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser
 225 230 235 240

Thr Gly Gly Thr Val Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr
 245 250 255

Ile Ser Tyr Glu Asp Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys
 260 265 270

Leu Val Val Lys Gly Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu
 275 280 285
 Asp Gln Gly Val Asp Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln
 290 295 300
 Leu Asp Arg Ala Pro Val Pro Phe His Leu Leu Pro Gln Val Arg Lys
 305 310 315 320
 Glu Val Gly Ser Glu Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn
 325 330 335
 Gly Ala Asp Ile Val Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu
 340 345 350
 Ile Gly Arg Ala Tyr Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly
 355 360 365
 Val Asp Arg Thr Ile Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met
 370 375 380
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 Ala Ala Glu Ile
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 Met Thr Gln Pro Gly
 1 5
 cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
 Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
 10 15 20
 gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
 Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
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 agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
 Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
 40 45 50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac	307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp	
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Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly	
70 75 80 85	
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Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile	
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Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu	
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Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu	
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Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile	
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Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln	
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Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val	
170 175 180	
aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc	691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu	
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Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
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Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
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Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
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Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
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Arg	Arg	Leu	Phe	Leu	Glu	Ala	Asp	Met	Pro	Leu	Pro	Ile	Ser	Gly	Glu		
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Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu	Lys	Tyr	Gly	Lys	Asp		
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Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala	Leu	Gln	Thr	Arg	Met		
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Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe	Ser	Lys	Ile	Pro	Gly		
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Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln	Ala	Met	Phe	Ser	Val		
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Leu	Pro	Asn	Gln	Leu	Pro	Lys	Arg	Met	Met	Glu	Tyr	Arg	Asn	Arg	Phe		
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Glu	His	His	Leu	Leu	Leu	Thr	Val	Ser	Glu	Ser	Gln	Lys	Ala	Ala	Ser		
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gag	aag	atg	ctc	aag	gag	ttc	ttc	gca	gag	ccc	gag	cac	act	ggt	gag	1363	
Glu	Lys	Met	Leu	Lys	Glu	Phe	Phe	Ala	Glu	Pro	Glu	His	Thr	Gly	Glu		
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ttc	ttc	atc	tgc	acg	tct	gat	gaa	gaa	aag	agc	gcg	tcg	ctc	aac	cgg	1411	
Phe	Phe	Ile	Cys	Thr	Ser	Asp	Glu	Glu	Lys	Ser	Ala	Ser	Leu	Asn	Arg		
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ttc	ggc	gcg	gcc	agt	gcc	gcc	act	cgc	tac	gcc	gcg	ttg	aag	cgc	cgg	1459	
Phe	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Arg	Tyr	Ala	Ala	Leu	Lys	Arg	Arg		
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cac	atc	gca	ggg	ctc	atc	ccc	atc	gat	gtg	gcc	ctg	cgt	cgc	gac	gat	1507	
His	Ile	Ala	Gly	Leu	Ile	Pro	Ile	Asp	Val	Ala	Leu	Arg	Arg	Asp	Asp		
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tgg	aac	tgg	ctc	gag	gtg	ctg	ccg	gag	gag	atc	gac	gac	cag	ctt	gag	1555	
Trp	Asn	Trp	Leu	Glu	Val	Leu	Pro	Glu	Glu	Ile	Asp	Asp	Gln	Leu	Glu		
470				475					480						485		
gtc	aag	gcg	tat	tac	ggg	cac	ttc	ttc	tgc	cat	gtg	atg	cac	cag	gac	1603	
Val	Lys	Ala	Tyr	Tyr	Gly	His	Phe	Phe	Cys	His	Val	Met	His	Gln	Asp		
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tat	gtc	gcc	aag	cag	ggc	gtg	gat	ctc	gag	gcg	ctg	cac	gac	cgc	atc	1651	
Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala	Leu	His	Asp	Arg	Ile		
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cag	cac	ctg	ctg	gag	gag	cgc	ggc	gcg	aag	ctg	ccc	gcc	gag	cac	aac	1699	
Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu	Pro	Ala	Glu	His	Asn		
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tac	ggt	cgc	atg	tac	aag	ctg	ccg	gag	tcc	atg	gaa	gag	cac	ttc	aag	1747	
Tyr	Gly	Arg	Met	Tyr	Lys	Leu	Pro	Glu	Ser	Met	Glu	Glu	His	Phe	Lys		

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gag	ctc	gat	ccg	acg	aat	acg	ttc	aac	gcc	ggt	atc	ggc	ggc	acg	tcg	1795
Glu	Leu	Asp	Pro	Thr	Asn	Thr	Phe	Asn	Ala	Gly	Ile	Gly	Gly	Thr	Ser	
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35 40 45

Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
50 55 60

Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
65 70 75 80

Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
85 90 95

Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
100 105 110

Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
115 120 125

Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
130 135 140

Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
145 150 155 160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
165 170 175

Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
180 185 190

Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
195 200 205

Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
210 215 220

Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
225 230 235 240

Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
 245 250 255
 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
 260 265 270
 Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
 275 280 285
 Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
 290 295 300
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
 305 310 315 320
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
 435 440 445
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
 450 455 460
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His
 485 490 495
 Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala
 500 505 510
 Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu
 515 520 525
 Pro Ala Glu His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met
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<213> Corynebacterium glutamicum

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cgc atc cag cac ttg ctg gag gag cac ggc aag aag ctg ccc gcc gag 96
Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
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cac aac tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac 144
His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
35 40 45

ttc aag gag ctc gat ccg acg aat acg ttc aac gcc ggt atc gcc gcc 192
Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
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Thr Ser Pro His Lys Asp Trp Ala
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<211> 72

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<213> Corynebacterium glutamicum

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Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
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Thr Ser Pro His Lys Asp Trp Ala
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                                         Met Thr Gln Pro Gly
                                         1 5
cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
          10          15          20
gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
          25          30          35
agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
          40          45          50
ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac 307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp
          55          60          65
aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt 355
Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly
          70          75          80          85
gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc 403
Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile
          90          95          100
tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag 451
Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu
          105          110          115
gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc 499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu
          120          125          130
gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc 547
Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile
          135          140          145
ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag 595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln
          150          155          160          165
att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc 643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val
          170          175          180
aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc 691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu
          185          190          195

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Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
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tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
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Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
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Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu	
295 300 305	
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Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp	
310 315 320 325	
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Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met	
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Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly	
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att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg	1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val	
360 365 370	
ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc	1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe	
375 380 385	
gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc	1315
Glu His His Leu Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser	
390 395 400 405	
gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag	1363
Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu	
410 415 420	
ttc ttc atc tgc acg tct gat gaa gaa aag agc gcg tcg ctc aac ccg	1411
Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg	
425 430 435	

ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg 1459
 Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg
 440 445 450
 cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat 1507
 His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp
 455 460 465
 tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag 1555
 Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu
 470 475 480 485
 gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac 1603
 Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp
 490 495 500
 tat gtc gcc aag cag ggc gtg gat ctc gag gcg ctg cac gac cgc atc 1651
 Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile
 505 510 515
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<212> PRT

<213> Corynebacterium glutamicum

<400> 142

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 35 40 45
 Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
 50 55 60
 Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
 65 70 75 80
 Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
 85 90 95
 Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
 100 105 110
 Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
 115 120 125
 Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
 130 135 140
 Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
 145 150 155 160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
 165 170 175
 Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
 180 185 190
 Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
 195 200 205
 Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
 210 215 220
 Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
 225 230 235 240
 Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
 245 250 255
 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
 260 265 270
 Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
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 Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
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 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
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 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
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 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
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 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His

485								490					495				
Val	Met	His	Gln	Asp	Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala		
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Leu	His	Asp	Arg	Ile	Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu		
515								520					525				
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<222> (101)..(1012)  
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				Met	Lys	Ile	Phe	Val								
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Gly	Phe	Gly	Asp	Tyr	Pro	Leu	Thr	Thr	Lys	Ala	Leu	Lys	Glu	Ala	Gly	
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gca	gaa	ata	gtg	gac	tcc	ctc	gaa	aaa	gcc	gag	ggg	ttt	gtc	ttc	act	211
Ala	Glu	Ile	Val	Asp	Ser	Leu	Glu	Lys	Ala	Glu	Gly	Phe	Val	Phe	Thr	
			25					30					35			
caa	aca	cca	ggc	aca	gaa	ttt	ccc	cta	ctt	ccc	gac	gga	gtg	agg	tgg	259
Gln	Thr	Pro	Gly	Thr	Glu	Phe	Pro	Leu	Leu	Pro	Asp	Gly	Val	Arg	Trp	
		40					45					50				
gtg	caa	ttt	ccc	aat	gcg	ggg	ctc	aac	gca	tat	ttc	aca	gct	ggg	cag	307
Val	Gln	Phe	Pro	Asn	Ala	Gly	Leu	Asn	Ala	Tyr	Phe	Thr	Ala	Gly	Gln	
	55					60					65					
att	gat	gac	aaa	cgc	cgg	tgg	tca	aat	gca	tca	ggg	gtg	tat	ggc	caa	355
Ile	Asp	Asp	Lys	Arg	Arg	Trp	Ser	Asn	Ala	Ser	Gly	Val	Tyr	Gly	Gln	
70					75					80					85	
cag	gta	gcc	gaa	gca	gca	atg	gct	ctt	ttg	ctg	gga	ctg	att	cat	atg	403
Gln	Val	Ala	Glu	Ala	Ala	Met	Ala	Leu	Leu	Leu	Gly	Leu	Ile	His	Met	
				90					95					100		
cac	ccc	acc	atg	gtg	cgt	gcc	gat	agt	tgg	gca	cca	agc	act	caa	ata	451
His	Pro	Thr	Met	Val	Arg	Ala	Asp	Ser	Trp	Ala	Pro	Ser	Thr	Gln	Ile	
			105					110					115			
gat	cag	cag	acc	aga	tgg	ctt	gat	ggg	gca	aca	gtt	gcc	att	gtg	gga	499
Asp	Gln	Gln	Thr	Arg	Trp	Leu	Asp	Gly	Ala	Thr	Val	Ala	Ile	Val	Gly	
	120						125					130				

gct ggt gga atc ggt aaa cat ctg gca gcc atg ttg aaa cct ttt ggc 547
 Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met Leu Lys Pro Phe Gly
 135 140 145

gca aag tct tta gca gta agc agg acc ggt aca ccc acc caa gat ttt 595
 Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr Pro Thr Gln Asp Phe
 150 155 160 165

gat gca acg gaa cct ata tcc aac ctg cac caa gta ctt gcc gac gcc 643
 Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln Val Leu Ala Asp Ala
 170 175 180

gac cat gtg gtg ttg tgc gta ccg ctt acc gca gac acc tat cat ctg 691
 Asp His Val Val Leu Cys Val Pro Leu Thr Ala Asp Thr Tyr His Leu
 185 190 195

atc gga aaa gca gag ctt aaa gca atg cag tcc act gca att ttg atc 739
 Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser Thr Ala Ile Leu Ile
 200 205 210

aac gtg gct cgc gga gaa gta gta gat aca gaa gca tta gtt gac gcc 787
 Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu Ala Leu Val Asp Ala
 215 220 225

tta gat gcc caa gaa ata tcc ggg gca ggc tta gat gtc acc gat cct 835
 Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu Asp Val Thr Asp Pro
 230 235 240 245

gaa cca ttg ccg gac gat cat cca ctg tgg ggg cgc agc aat gtg atc 883
 Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly Arg Ser Asn Val Ile
 250 255 260

att acc ccg cac gta gcc aac acg ttg acc tcg atg gat cgc atg ctt 931
 Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser Met Asp Arg Met Leu
 265 270 275

gcc cca gtg gtg gca gaa aac tac cga cgg ttt ctc gct gga gaa aag 979
 Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe Leu Ala Gly Glu Lys
 280 285 290

atg ctg acc gag gtg gac atc cac aaa ggt tac tagagcagtg gctttgaata 1032
 Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
 295 300

tag 1035

<210> 144

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Lys Ile Phe Val Gly Phe Gly Asp Tyr Pro Leu Thr Thr Lys Ala
 1 5 10 15

Leu Lys Glu Ala Gly Ala Glu Ile Val Asp Ser Leu Glu Lys Ala Glu
 20 25 30

Gly Phe Val Phe Thr Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro
 35 40 45

Asp Gly Val Arg Trp Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr
 50 55 60
 Phe Thr Ala Gly Gln Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser
 65 70 75 80
 Gly Val Tyr Gly Gln Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu
 85 90 95
 Gly Leu Ile His Met His Pro Thr Met Val Arg Ala Asp Ser Trp Ala
 100 105 110
 Pro Ser Thr Gln Ile Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr
 115 120 125
 Val Ala Ile Val Gly Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met
 130 135 140
 Leu Lys Pro Phe Gly Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr
 145 150 155 160
 Pro Thr Gln Asp Phe Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln
 165 170 175
 Val Leu Ala Asp Ala Asp His Val Val Leu Cys Val Pro Leu Thr Ala
 180 185 190
 Asp Thr Tyr His Leu Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser
 195 200 205
 Thr Ala Ile Leu Ile Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu
 210 215 220
 Ala Leu Val Asp Ala Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu
 225 230 235 240
 Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly
 245 250 255
 Arg Ser Asn Val Ile Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser
 260 265 270
 Met Asp Arg Met Leu Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe
 275 280 285
 Leu Ala Gly Glu Lys Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
 290 295 300

<210> 145

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (62)..(664)

<223> RXN01130

<400> 145

agttcgtggc ggaatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60

gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
 Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1 5 10 15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
 Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
 20 25 30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
 Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
 35 40 45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
 Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
 50 55 60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
 Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
 65 70 75 80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
 Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
 85 90 95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
 Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
 100 105 110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
 Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
 115 120 125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
 Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
 130 135 140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
 Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
 145 150 155 160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
 Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
 165 170 175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
 Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
 180 185 190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
 Ala Thr Ser Phe Gln Val Asp Leu Asp
 195 200

tga 687

<210> 146

<211> 201
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 146

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Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1             5             10             15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
      20             25             30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
      35             40             45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
      50             55             60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
      65             70             75             80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
      85             90             95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
      100            105            110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
      115            120            125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
      130            135            140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
      145            150            155            160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
      165            170            175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
      180            185            190

Ala Thr Ser Phe Gln Val Asp Leu Asp
      195            200
  
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<210> 147
 <211> 326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(303)
 <223> FRXA01130

<400> 147

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gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag atc acc cgc atc   48
Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
 1             5             10             15

aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg   96
  
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Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
      20                      25                      30

cag tac act gac gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg   144
Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
      35                      40                      45

ggt gct gct ggc atc aac atc gag gct gct gcg ttg act cag gct gag   192
Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
      50                      55                      60

aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tct   240
Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
      65                      70                      75                      80

gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt gct act tcc ttc   288
Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
      85                      90                      95

cag gtt gat ctt gac taattagaga tccatttgct tga   326
Gln Val Asp Leu Asp
      100

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<210> 148
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 148
Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
  1           5           10           15

Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
      20                      25                      30

Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
      35                      40                      45

Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
      50                      55                      60

Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
      65                      70                      75                      80

Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
      85                      90                      95

Gln Val Asp Leu Asp
      100

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<210> 149
 <211> 604
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(604)
 <223> RXN03112

<400> 149

gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgcgtagag ggcgagtga agcggctcttc tttcaacggt gtg gaa att ttc gga 115
 Val Glu Ile Phe Gly
 1 5

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
 Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
 10 15 20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
 Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
 25 30 35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
 Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
 40 45 50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
 Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
 55 60 65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
 Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
 70 75 80 85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
 Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
 90 95 100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
 Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
 105 110 115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
 Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
 120 125 130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
 Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
 135 140 145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
 Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
 150 155 160 165

gcg ctg gct 604
 Ala Leu Ala

<210> 150

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
 1 5 10 15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
 20 25 30
 Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
 35 40 45
 Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr
 50 55 60
 Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His
 65 70 75 80
 Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg
 85 90 95
 Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly
 100 105 110
 His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr
 115 120 125
 Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu
 130 135 140
 Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala
 145 150 155 160
 Asp Ser Val Leu Lys Ala Leu Ala
 165

<210> 151
 <211> 649
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(649)
 <223> FRXA01133

<400> 151
 tgttttctagt cgcacgccaa aacccggcgt ggacacgtct gcagccgacg cggtcgtgcc 60
 tgttgtagac ggacattcct agtttttcca ggagtaactt gtg agc cag aat ggc 115
 Val Ser Gln Asn Gly
 1 5
 cgt ccg gta gtc ctc atc gcc gat aag ctt gcg cag tcc act gtt gac 163
 Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala Gln Ser Thr Val Asp
 10 15 20
 gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac gga cct aac cgc 211
 Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro Asn Arg
 25 30 35
 cca gaa ctg ctt gat gca gtt aag gaa gcg gac gca ctg ctc gtg cgt 259
 Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp Ala Leu Leu Val Arg
 40 45 50

tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg 307
 Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu
 55 60 65

aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct 355
 Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro
 70 75 80 85

gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat 403
 Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn
 90 95 100

att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct 451
 Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala
 105 110 115

cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc 499
 Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser
 120 125 130

ggt ctt ctt tca acg gtg tgg aaa ttt tcg gaa aaa ctg tcg gta tcg 547
 Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser
 135 140 145

tcg gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt 595
 Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg
 150 155 160 165

ttg aga cca cca ttg ttg ctt acg atc ctt acg cta acc ctg ctt cgt 643
 Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr Leu Thr Leu Leu Arg
 170 175 180

gcg ggt
 Ala Gly 649

<210> 152

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Val Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
 1 5 10 15

Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
 20 25 30

Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
 35 40 45

Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
 50 55 60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65 70 75 80

Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
 85 90 95

Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
 100 105 110

Leu Leu Ser Thr Ala Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val
 115 120 125

Arg Ala Ser Gly Ser Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu
 130 135 140

Lys Leu Ser Val Ser Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu
 145 150 155 160

Ser Val Leu Leu Arg Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr
 165 170 175

Leu Thr Leu Leu Arg Ala Gly
 180

<210> 153
 <211> 1011
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(988)
 <223> RXN00871

<400> 153
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gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
 Met Arg Trp Phe His
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
 70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
 Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
 90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451

Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
105 110 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
120 125 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
135 140 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
150 155 160 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
170 175 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
185 190 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser
200 205 210

cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc 787
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile
215 220 225

gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc 835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly
230 235 240 245

tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga 883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg
250 255 260

atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca 931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr
265 270 275

tgg acc ggg caa gca ttt gat gat cgc ttg cca tat gag aac gca aac 979
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro Tyr Glu Asn Ala Asn
280 285 290

aag gag gga taaaatttca tggctgaaac gaa 1011
Lys Glu Gly
295

<210> 154

<211> 296

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln
1 5 10 15

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
 20 25 30
 Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
 35 40 45
 Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
 50 55 60
 His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
 65 70 75 80
 Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
 85 90 95
 Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
 100 105 110
 Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
 115 120 125
 Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
 130 135 140
 Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
 145 150 155 160
 Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
 165 170 175
 His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285
 Tyr Glu Asn Ala Asn Lys Glu Gly
 290 295

<210> 155

<211> 964

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> FRXA00871

<400> 155

gggaaaaggc gatcaccagc cggtggctcg acccagcaac ccacggtggc attaacctcg 60

gtttccca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
 Met Arg Trp Phe His
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
 70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
 Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
 90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451
 Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
 105 110 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
 Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
 120 125 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
 Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
 135 140 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
 Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
 150 155 160 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
 Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
 170 175 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
 Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
 185 190 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
 Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser

200	205	210	
cca gcg ggg gag atc gat	atc aac gcc atg gtg tac agc ggc gat atc		787
Pro Ala Gly Glu Ile Asp	Ile Asn Ala Met Val Tyr Ser Gly Asp Ile		
215	220	225	
gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc			835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly			
230	235	240	245
tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga			883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg			
250	255	260	
atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca			931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr			
265	270	275	
tgg acc ggg caa gca ttt gat gat cgc ttg cca			964
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro			
280	285		

<210> 156

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln	
1 5 10 15	
Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg	
20 25 30	
Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly	
35 40 45	
Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His	
50 55 60	
His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly	
65 70 75 80	
Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser	
85 90 95	
Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys	
100 105 110	
Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly	
115 120 125	
Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala	
130 135 140	
Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu	
145 150 155 160	
Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly	
165 170 175	

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190

Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285

<210> 157
 <211> 373
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(373)
 <223> RXN02829

<400> 157
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ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
 Met Gln Lys Asn Ile
 1 5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
 10 15 20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
 25 30 35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
 40 45 50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
 Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
 55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
 Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp

70 75 80 85

gga cat atg acg tgg gat 373
 Gly His Met Thr Trp Asp
 90

<210> 158
 <211> 91
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 158
 Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
 1 5 10 15
 Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
 20 25 30
 Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
 35 40 45
 Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
 50 55 60
 Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
 65 70 75 80
 Arg Leu Thr Asp Asp Gly His Met Thr Trp Asp
 85 90

<210> 159
 <211> 376
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(376)
 <223> FRXA02829

<400> 159
 tttttcgttt aatctcatat ttaaacacgt tccttttaat tggttttata aattgataaa 60
 ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
 Met Gln Lys Asn Ile
 1 5
 cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
 10 15 20
 tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
 25 30 35
 gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
 40 45 50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
70 75 80 85

gga cat atg acg tgg gga tcc 376
Gly His Met Thr Trp Gly Ser
90

<210> 160

<211> 92

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
1 5 10 15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
20 25 30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
35 40 45

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
50 55 60

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
65 70 75 80

Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser
85 90

<210> 161

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (925)

<223> RXN01468

<400> 161

tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacagggg caatggtgtt atg aca gtg aac att 115
Met Thr Val Asn Ile
1 5

tca	tat	ctg	acc	gac	atg	gac	ggc	gtc	ctc	atc	aaa	gag	ggc	gag	ata	163
Ser	Tyr	Leu	Thr	Asp	Met	Asp	Gly	Val	Leu	Ile	Lys	Glu	Gly	Glu	Ile	
				10					15					20		

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val

tagtattctg taggtcatgg cat

948

<210> 162

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
 1 5 10 15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
275

<210> 163

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> FRXA01468

<400> 163

tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacagga caatggtgtt atg aca gtg aac att 115
Met Thr Val Asn Ile
1 5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
10 15 20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val
25 30 35

gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt 259
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu
40 45 50

tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att 307
Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile
55 60 65

tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag 355
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys
70 75 80 85

gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg 403
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu
90 95 100

cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc 451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val
105 110 115

ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata 499
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile
120 125 130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc 547
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val
135 140 145

act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc 595
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala
150 155 160 165

gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag 643
 Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys
 170 175 180
 cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat 691
 Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His
 185 190 195
 tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa 739
 Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys
 200 205 210
 tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att 787
 Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile
 215 220 225
 tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg 835
 Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val
 230 235 240 245
 atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt 883
 Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly
 250 255 260
 gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac 925
 Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp
 265 270 275
 tagtattctg taggtcatgg cat 948

<210> 164

<211> 275

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 164

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
 1 5 10 15
 Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30
 Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45
 Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60
 Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80
 Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95
 Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110
 Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
 275

<210> 165
 <211> 1128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1105)
 <223> RXA00794

<400> 165
 gcgggttgat acagcccaag cgccgataca tttataatgc gcctagatac gtgcaaccga 60

cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115
 Met Asn Leu Lys Asn
 1 5

ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163
 Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr
 10 15 20

gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211
 Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys
 25 30 35

aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259
 Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn
 40 45 50

tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac 307

Ser	Val	Thr	Met	Lys	Gly	Val	Val	Val	Ile	Gly	Glu	Gly	Glu	Lys	Asp		
55						60					65						
gaa gct cca atg ctg tac aac ggc gaa gag gtc gga acc ggc ttt gga 355																	
Glu	Ala	Pro	Met	Leu	Tyr	Asn	Gly	Glu	Glu	Val	Gly	Thr	Gly	Phe	Gly		
70					75					80					85		
cct gag gtt gat atc gca gtt gac cca gtt gac ggc acc acc ctg atg 403																	
Pro	Glu	Val	Asp	Ile	Ala	Val	Asp	Pro	Val	Asp	Gly	Thr	Thr	Leu	Met		
				90					95					100			
gct gag ggt cgc ccc aac gca att tcc att ctc gca gct gca gag cgt 451																	
Ala	Glu	Gly	Arg	Pro	Asn	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Ala	Glu	Arg		
			105					110					115				
ggc acc atg tac gat cca tcc tcc gtc ttc tac atg aag aag atc gcc 499																	
Gly	Thr	Met	Tyr	Asp	Pro	Ser	Ser	Val	Phe	Tyr	Met	Lys	Lys	Ile	Ala		
		120					125					130					
gtg gga cct gag gcc gca ggc aag atc gac atc gaa gct cca gtt gcc 547																	
Val	Gly	Pro	Glu	Ala	Ala	Gly	Lys	Ile	Asp	Ile	Glu	Ala	Pro	Val	Ala		
		135				140					145						
cac aac atc aac gcg gtg gca aag tcc aag gga atc aac cct tcc gac 595																	
His	Asn	Ile	Asn	Ala	Val	Ala	Lys	Ser	Lys	Gly	Ile	Asn	Pro	Ser	Asp		
150					155					160					165		
gtc acc gtt gtc gtg ctt gac cgt cct cgc cac atc gaa ctg atc gca 643																	
Val	Thr	Val	Val	Val	Leu	Asp	Arg	Pro	Arg	His	Ile	Glu	Leu	Ile	Ala		
				170					175					180			
gac att cgt cgt gca ggc gca aag gtt cgt ctc atc tcc gac ggc gac 691																	
Asp	Ile	Arg	Arg	Ala	Gly	Ala	Lys	Val	Arg	Leu	Ile	Ser	Asp	Gly	Asp		
			185					190					195				
gtt gca ggt gca gtt gca gca gct cag gat tcc aac tcc gtg gac atc 739																	
Val	Ala	Gly	Ala	Val	Ala	Ala	Ala	Gln	Asp	Ser	Asn	Ser	Val	Asp	Ile		
		200					205					210					
atg atg ggc acc ggc gga acc cca gaa ggc atc atc act gcg tgc gcc 787																	
Met	Met	Gly	Thr	Gly	Gly	Thr	Pro	Glu	Gly	Ile	Ile	Thr	Ala	Cys	Ala		
		215				220					225						
atg aag tgc atg ggt ggc gaa atc cag ggc atc ctg gcc cca atg aac 835																	
Met	Lys	Cys	Met	Gly	Gly	Glu	Ile	Gln	Gly	Ile	Leu	Ala	Pro	Met	Asn		
230					235					240					245		
gat ttc gag cgc cag aag gca cac gac gct ggt ctg gtt ctt gat cag 883																	
Asp	Phe	Glu	Arg	Gln	Lys	Ala	His	Asp	Ala	Gly	Leu	Val	Leu	Asp	Gln		
				250					255					260			
gtt ctg cac acc aac gat ctg gtg agc tcc gac aac tgc tac ttc gtg 931																	
Val	Leu	His	Thr	Asn	Asp	Leu	Val	Ser	Ser	Asp	Asn	Cys	Tyr	Phe	Val		
				265				270					275				
gca acc ggt gtg acc aac ggt gac atg ctc cgt ggc gtt tcc tac cgc 979																	
Ala	Thr	Gly	Val	Thr	Asn	Gly	Asp	Met	Leu	Arg	Gly	Val	Ser	Tyr	Arg		
		280					285					290					
gca aac ggc gca acc acc cgt tcc ctg gtt atg cgc gca aag tca ggc 1027																	
Ala	Asn	Gly	Ala	Thr	Thr	Arg	Ser	Leu	Val	Met	Arg	Ala	Lys	Ser	Gly		

295 300 305
 acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa 1075
 Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu
 310 315 320 325
 tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa 1125
 Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 330 335
 aac 1128
 <210> 166
 <211> 335
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 166
 Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu
 1 5 10 15
 Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val
 20 25 30
 Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met
 35 40 45
 Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly
 50 55 60
 Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val
 65 70 75 80
 Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp
 85 90 95
 Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu
 100 105 110
 Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr
 115 120 125
 Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile
 130 135 140
 Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly
 145 150 155 160
 Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His
 165 170 175
 Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu
 180 185 190
 Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Gln Asp Ser
 195 200 205
 Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile
 210 215 220

Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile
 225 230 235 240

Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly
 245 250 255

Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp
 260 265 270

Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg
 275 280 285

Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met
 290 295 300

Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu
 305 310 315 320

Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 325 330 335

<210> 167
 <211> 1035
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> RXN02920

<400> 167
 tgc atg caga ttatctgtcc aactacgccca gccgcgcgta aagcgcgggc ctgctggtgg 60

cgggtggcgt cgaaaagcat ttttaaagga gtttaagacg atg aag ttt gtt atg 115
 Met Lys Phe Val Met
 1 5

tat ccg cat ttg tgg gag tcc acg acc gct gtc att gag ggt ggc gga 163
 Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val Ile Glu Gly Gly Gly
 10 15 20

cat gag cgg gtt gag gat att aaa gat gca gac ttc att ttc ttt aat 211
 His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp Phe Ile Phe Phe Asn
 25 30 35

ggt tca gcg ccg gag ttc ccg gat ttg ccg gag aac atc aag ttc gtg 259
 Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu Asn Ile Lys Phe Val
 40 45 50

cag gcc tcc atg gcg ggt att gat gcg ctg gtc aag cgt ggt gtc gtc 307
 Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val Lys Arg Gly Val Val
 55 60 65

aat gag aag gca cgt tgg gca aac gcg gct ggc ctg tac gct gac acc 355
 Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
 70 75 80 85

gtt gct gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat 403
 Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His

90	95	100	
gcg acg act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu 105 110 115			451
aac aac aag tca tgg ctg cat gac aat aaa act gtc gct att ttg ggc Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly 120 125 130			499
gcc ggt ggc att ggc gtg cgt ctg ctg gaa atg ctc aag ccg ttc aac Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn 135 140 145			547
gtg aag acc att gcg gtt aat aac tct ggt cgt ccg gtg gaa ggt gca Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala 150 155 160 165			595
gat gaa acc ttc gcc atg gat aag gct gag cac gtg tgg gct gag gct Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala 170 175 180			643
gat gtg ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile 185 190 195			691
gtc aat gca gaa act ttg ggc aag atg aag cct tct gcc gtg gtg gtc Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val 200 205 210			739
aat gtg ggg cgt ggc ccg ctg atc aac acc gat gat ctg gtg gat gca Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala 215 220 225			787
ttg aac aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro 230 235 240 245			835
gag cca ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val 250 255 260			883
atc act cct cat act gca aac acg aat gag agg att cgt gct ttg acc Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr 265 270 275			931
ggc gaa ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln 280 285 290			979
atg gcc acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr 295 300			1032
ccg			1035

<210> 168

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 168
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 Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp
 20 25 30
 Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu
 35 40 45
 Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val
 50 55 60
 Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly
 65 70 75 80
 Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala
 85 90 95
 Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val
 100 105 110
 Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr
 115 120 125
 Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met
 130 135 140
 Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg
 145 150 155 160
 Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His
 165 170 175
 Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp
 180 185 190
 Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro
 195 200 205
 Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp
 210 215 220
 Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu
 225 230 235 240
 Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu
 245 250 255
 Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg
 260 265 270
 Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe
 275 280 285
 Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 290 295 300


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<220>  
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<222> (52) .. (756)  
<223> FRXA02379
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249

ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt atc act 633
 Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val Ile Thr
 180 185 190

cct cat act gca aac acg aat gag agg att cgt gct ttg acc ggc gaa 681
 Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr Gly Glu
 195 200 205 210

ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag atg gcc 729
 Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln Met Ala
 215 220 225

acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 776
 Thr Glu Val Asp Val Val Ala Gly Tyr
 230 235

ccg 779

<210> 170

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Met Arg Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
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Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His
 20 25 30

Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu
 35 40 45

Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly
 50 55 60

Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn
 65 70 75 80

Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala
 85 90 95

Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala
 100 105 110

Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
 115 120 125

Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
 130 135 140

Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
 145 150 155 160

Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
 165 170 175

Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
 180 185 190

Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
 195 200 205
 Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
 210 215 220
 Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 225 230 235

<210> 171
 <211> 792
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(769)
 <223> RXN02688

<400> 171
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 gggttcgcgc agcaagcgaa ggaaggaaac ttaactagcc atg gcc gcc cgg att 115
 Met Ala Gly Arg Ile
 1 5
 att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163
 Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
 10 15 20
 gac acc cgc cca cca gga gct gaa ctc acc gac ctg gcc cgt aaa caa 211
 Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
 25 30 35
 gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259
 Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
 40 45 50
 gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307
 Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
 55 60 65
 ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg 355
 Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
 70 75 80 85
 att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc gcc gac 403
 Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
 90 95 100
 ttt gaa atg cgc gcc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451
 Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
 105 110 115
 ctc aac gcc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc gcc ggt 499
 Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
 120 125 130
 gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga 547
 Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg

135 140 145

atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc 595
 Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
 150 155 160 165

agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg 643
 Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
 170 175 180

gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg 691
 Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
 185 190 195

gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc 739
 Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
 200 205 210

tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg 789
 Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
 215 220

gat 792

<210> 172
 <211> 223
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 172
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Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
 20 25 30

Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
 35 40 45

Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
 50 55 60

Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
 65 70 75 80

Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
 85 90 95

Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
 100 105 110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
 115 120 125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
 130 135 140

Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
 145 150 155 160

Asp	Val	Ala	Val	Val	Ser	His	Gly	Ala	Val	Ile	Arg	Ile	Val	Ala	Thr
				165					170					175	
His	Ala	Thr	Gly	Val	Asp	Pro	Asn	Phe	Ala	Phe	Asn	Thr	Tyr	Leu	Gly
			180					185					190		
Asn	Cys	Arg	Phe	Val	Val	Leu	Glu	Pro	Asn	Gly	Lys	Lys	Phe	Ser	Gln
		195					200					205			
Trp	Asp	Val	Val	Arg	Trp	Thr	Asp	Ser	Pro	Leu	Pro	Trp	Gln	Glu	
	210					215					220				

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<211> 336
<212> DNA
<213> Corynebacterium glutamicum

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<220>  
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<223> RXN03087
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<400> 173
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gaatacctgg aaaagagctg atattgatag ggtttaagtc atg aag atc tac gca 115
Met Lys Ile Tyr Ala
1 5

cct ttt gct gga atc gtc cac tat ttt gtc gat gaa ggc gat ccc gtg 163
Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp Glu Gly Asp Pro Val
10 15 20

gaa acc ggc atg caa ctg gga acg gta gaa acc atc aaa ctc gag gca 211
Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr Ile Lys Leu Glu Ala
25 30 35

cca atc atg gca ccg gga cct ggc atc gta gct aag gtt tct ttt gat 259
Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala Lys Val Ser Phe Asp
40 45 50

gat ttc tcc gac gtc acc ggc ggc gat gaa ctc ctc gaa ttg gag gca 307
Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu Leu Glu Leu Glu Ala
55 60 65

aag aac taatgggtca aaccgcgcatc att 336
Lys Asn
70

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<210> 174
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 174
Met Lys Ile Tyr Ala Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp
1 5 10 15
Glu Gly Asp Pro Val Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr

20 25 30
 Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala
 35 40 45
 Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu
 50 55 60
 Leu Glu Leu Glu Ala Lys Asn
 65 70

<210> 175
 <211> 310
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(310)
 <223> RXN03186

<400> 175
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 cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
 Met Ala Asp Gln Ala
 1 5
 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20
 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35
 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50
 cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65
 cgc 310
 Arg
 70

<210> 176
 <211> 70
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 176
 Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
 1 5 10 15
 Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
 20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60

Arg Ala Ser Ala Lys Arg
 65 70

<210> 177

<211> 302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(279)

<223> RXN03187

<400> 177

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 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45

tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60

gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90

caagggacag ata 302

<210> 178

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
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Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90

<210> 179
 <211> 1953
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1930)
 <223> RXN02591

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 Met Thr Thr Ala Ala
 1 5
 atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg 163
 Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu
 10 15 20
 aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg 211
 Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val
 25 30 35
 ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt 259
 Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu
 40 45 50
 gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac 307
 Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn
 55 60 65
 agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc 355
 Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser
 70 75 80 85
 cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac 403
 Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn
 90 95 100
 aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac 451
 Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr
 105 110 115
 gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg 499
 Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met
 120 125 130

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac	547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp	
135 140 145	
tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att	595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile	
150 155 160 165	
gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc	643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu	
170 175 180	
cac tcc gtt ggt gct cct atg gag cca ggc cag gaa gac gtt gca tgg	691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp	
185 190 195	
cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa	739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu	
200 205 210	
att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag	787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys	
215 220 225	
aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga	835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly	
230 235 240 245	
tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc	883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly	
250 255 260	
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc	931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr	
265 270 275	
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt	979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val	
280 285 290	
gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac	1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr	
295 300 305	
gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac	1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn	
310 315 320 325	
tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc	1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr	
330 335 340	
ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa	1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu	
345 350 355	
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac	1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn	
360 365 370	

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt	1267
Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg	
375 380 385	
tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac	1315
Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn	
390 395 400 405	
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Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg	
410 415 420	
gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc	1411
Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly	
425 430 435	
acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca	1459
Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala	
440 445 450	
gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca	1507
Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro	
455 460 465	
ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg	1555
Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met	
470 475 480 485	
ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg	1603
Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp	
490 495 500	
ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac	1651
Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp	
505 510 515	
aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt	1699
Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val	
520 525 530	
ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc	1747
Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu	
535 540 545	
gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg	1795
Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu	
550 555 560 565	
acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag	1843
Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu	
570 575 580	
tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag	1891
Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln	
585 590 595	
ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac	1940
Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala	
600 605 610	
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<210> 180

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

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Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
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Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
 35 40 45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
 50 55 60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65 70 75 80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
 85 90 95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
 100 105 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
 115 120 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
 130 135 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
 145 150 155 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
 165 170 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
 180 185 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
 195 200 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
 210 215 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
 225 230 235 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
 245 250 255

Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
 260 265 270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
 275 280 285

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
 290 295 300
 Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
 305 310 315 320
 Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
 325 330 335
 Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
 340 345 350
 Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
 355 360 365
 Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
 370 375 380
 His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
 385 390 395 400
 Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
 405 410 415
 Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
 420 425 430
 Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
 435 440 445
 Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
 450 455 460
 Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
 465 470 475 480
 Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
 485 490 495
 Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
 500 505 510
 Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
 515 520 525
 Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
 530 535 540
 Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
 545 550 555 560
 Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
 565 570 575
 Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
 580 585 590
 Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
 595 600 605

His Ala
610

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<223> RXS01260

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Val Thr Phe Asn Tyr
1 5

gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
10 15 20

ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
25 30 35

ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
40 45 50

gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
55 60 65

tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
70 75 80 85

tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
90 95 100

att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
105 110 115

aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt 499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu
120 125 130

cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag 547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
135 140 145

aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg 595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
150 155 160 165

gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
200 205 210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
250 255 260	
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
265 270 275	
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala	
280 285 290	
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc	1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe	
295 300 305	
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca	1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala	
310 315 320 325	
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg	1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu	
330 335 340	
gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag	1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln	
345 350 355	
aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac	1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His	
360 365 370	
cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga	1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly	
375 380 385	
cac atg atc aac ttc tagaatccac ctggttgccc ctg	1305
His Met Ile Asn Phe	
390	

gcg ttg ggt gat ttg gcg gag gta acc aag ttg aag gtg cgc. caa tcc	883
Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu Lys Val Arg Gln Ser	
250 255 260	
aag gga gtg cat ttg ctc act ggt gat ttg ggc agc cag agt ggc gtg	931
Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly Ser Gln Ser Gly Val	
265 270 275	
ttt gtg cgt ggc aaa aac ggc aag cat gtg atc gtg aat ccg tgg atg	979
Phe Val Arg Gly Lys Asn Gly Lys His Val Ile Val Asn Pro Trp Met	
280 285 290	
ggg cgc acc ctt att ggt cca acc gac acc atg att gac ggt gac gct	1027
Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met Ile Asp Gly Asp Ala	
295 300 305	
gat gat gcg gct gca gat gaa agc gat atc gat ttg ctg ctt gag acc	1075
Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp Leu Leu Leu Glu Thr	
310 315 320 325	
atc gat tcg gta cgc gct aca ccg ctt gat cgc aaa gag atc atc tcc	1123
Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg Lys Glu Ile Ile Ser	
330 335 340	
acg ctg gtg ggt gtg cgc ccg ctt gtt gat gac ggc acc gac acc tac	1171
Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp Gly Thr Asp Thr Tyr	
345 350 355	
acg tcc tct cgc cgt ttc gat att tcc gat cac gcc aac gtc ggc att	1219
Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile	
360 365 370	
gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg	1267
Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val	
375 380 385	
atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg	1315
Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val	
390 395 400 405	
tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act	1363
Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr	
410 415 420	
tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt	1411
Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu	
425 430 435	
cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg	1459
Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu	
440 445 450	
gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca	1507
Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala	
455 460 465	
aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc	1555
Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile	
470 475 480 485	

	1	5	
ttt gaa tcc cgc cgg att ggc cct ccg ctt cgc gat aat tat gac gtc			163
Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val	10	20	
att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct			211
Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala	25	30	35
caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct			259
Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser	40	45	50
tct gga aca tca tcg aca acc tcc aag atg att cat ggt ggt ttg cgc			307
Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg	55	60	65
tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa			355
Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu	70	75	80
cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt			403
Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser	90	95	100
ttc atg ctc acg gcg ttt gat tgg tca gag ccg aaa gcc cct atg ttg			451
Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu	105	110	115
ggt gct ggt gtg gcg ttg tat gaa acg atg gcg tgg cag cgt aac cag			499
Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala Trp Gln Arg Asn Gln	120	125	130
ggg caa tcg aag gaa aac cac tcg ccg cgt ttc cgg tgg att cct aaa			547
Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe Arg Trp Ile Pro Lys	135	140	145
aat gca ctg ctc aag gaa gtc ccg tgg ctt gac ccg gag ggc ttg aag			595
Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp Pro Glu Gly Leu Lys	150	155	160
gga gcg tgg cgc cac gat gat acg ttg aat ctc cat gca gaa cga ctc			643
Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu His Ala Glu Arg Leu	170	175	180
ctc ctc gcg gtg att aaa gct ttt gcg gca gat ggc gga acg gcg atc			691
Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp Gly Gly Thr Ala Ile	185	190	195
aac cac gcc aaa gtc act cgc att ctc cgg aac gtg gaa gaa ggc cgc			739
Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn Val Glu Glu Gly Arg	200	205	210
gtc aag ggt gta gaa gtg act gat cag gtc acc aac acc acg cat gag			787
Val Lys Gly Val Glu Val Thr Asp Gln Val Thr Asn Thr Thr His Glu	215	220	225
gtg aat gcc cct gtg gtg atc aac gct gcg ggt ccg tgg gtt gcg cag			835
Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly Pro Trp Val Ala Gln	230	235	240
			245

Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
85 90 95

Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
100 105 110

His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
115 120 125

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
130 135 140

Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
145 150 155 160

Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
165 170 175

Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
180 185 190

Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
195 200 205

Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
210 215 220

Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
225 230 235 240

Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
245 250 255

Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
260 265 270

Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
275 280 285

Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
290 295 300

Gln
305

<210> 191
<211> 1809
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1786)
<223> RXA01851

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cacgatgtgg gttggcggtt ttcctattag gctcactttt atg acg agc gca cac 115
Met Thr Ser Ala His

Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln
 150 155 160 165

gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg 643
 Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val
 170 175 180

gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc 691
 Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala
 185 190 195

tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg 739
 Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser
 200 205 210

ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg 787
 Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu
 215 220 225

ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg 835
 Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu
 230 235 240 245

gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag 883
 Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu
 250 255 260

cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat 931
 Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn
 265 270 275

ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt 979
 Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu
 280 285 290

gcc acc aag ctt ggt gtg gag atg ccg atc acc cag 1015
 Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln
 295 300 305

<210> 190

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu
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 20 25 30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80

Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met
 305 310 315 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu
 325 330

<210> 189

<211> 1015

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> FRXA01025

<400> 189

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ctgaracggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc 115
 Val Val Ser Val Ser
 1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
 10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
 Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
 25 30 35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
 Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
 40 45 50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
 Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
 55 60 65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
 Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
 70 75 80 85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
 Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
 90 95 100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg ccg atg agt 451
 Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
 105 110 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499
 Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
 120 125 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547
 Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
 135 140 145

gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag 595

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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 20 25 30
 Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45
 Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60
 Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80
 Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
 85 90 95
 Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
 100 105 110
 His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
 115 120 125
 Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
 130 135 140
 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
 145 150 155 160
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
 165 170 175
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
 180 185 190
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
 195 200 205
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
 210 215 220
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
 225 230 235 240
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
 245 250 255
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
 260 265 270
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
 275 280 285
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
 290 295 300

105	110	115	
gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val 120	125	130	499
ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala 135	140	145	547
gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln 150	155	160	595
gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val 170	175	180	643
gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala 185	190	195	691
tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser 200	205	210	739
ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu 215	220	225	787
ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu 230	235	240	835
gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu 250	255	260	883
cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn 265	270	275	931
ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu 280	285	290	979
gcc acc aag ctt ggt gtg gag atg ccg atc acc cag gct gtc tac ggt Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln Ala Val Tyr Gly 295	300	305	1027
gtg tgc cac cga gat atg aaa gta act gac atg att gtg gct ctc atg Val Cys His Arg Asp Met Lys Val Thr Asp Met Ile Val Ala Leu Met 310	315	320	1075
ggc agg tct aag aag gct gag tagtcttagg ttgtaagctt caa Gly Arg Ser Lys Lys Ala Glu 330			1119

<210> 188

<211> 332

420	425	430
Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val		
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Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly		
450	455	460
Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys		
465	470	480
Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala		
485	490	495
Glu Trp Asn Arg Ala Val Glu His Ser Tyr Asp Gln Ala		
500	505	

<210> 187

<211> 1119

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1096)

<223> RXN01025

<400> 187

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ctgagacggt taaatatcgt ttctgaaagg tgggtttcgc	gtg gtt tct gta agc	115
	Val Val Ser Val Ser	
	1 5	

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct	163
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser	
10 15 20	

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca	211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala	
25 30 35	

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att	259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile	
40 45 50	

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta	307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu	
55 60 65	

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt	355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg	
70 75 80 85	

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg	403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu	
90 95 100	

gtg tcc ttg gct aaa ggt att gaa aaq ggc acg cac ctg cgg atg agt	451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser	

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr
 100 105 110
 Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp
 115 120 125
 Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys
 130 135 140
 Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
 145 150 155 160
 Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
 165 170 175
 Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
 180 185 190
 Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr
 195 200 205
 Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
 210 215 220
 Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
 225 230 235 240
 His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp
 245 250 255
 Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala
 260 265 270
 Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr
 275 280 285
 Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln
 290 295 300
 Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met
 305 310 315 320
 Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro
 325 330 335
 Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly
 340 345 350
 Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp
 355 360 365
 Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn
 370 375 380
 Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr
 385 390 395 400
 Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu
 405 410 415
 Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln

ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc 1267
 Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala
 375 380 385
 cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac 1315
 Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp
 390 395 400 405
 gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac 1363
 Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp
 410 415 420
 ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc 1411
 Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe
 425 430 435
 ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc 1459
 Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val
 440 445 450
 ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act 1507
 Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr
 455 460 465
 gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac 1555
 Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp
 470 475 480 485
 atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala
 490 495 500
 gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650
 Val Glu His Ser Tyr Asp Gln Ala
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<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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 20 25 30
 Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp
 35 40 45
 Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val
 50 55 60
 Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser
 65 70 75 80
 Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His
 85 90 95

ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc	547
Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu	
135 140 145	
gac aac gtt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg	595
Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu	
150 155 160 165	
ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc	643
Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val	
170 175 180	
cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac	691
Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn	
185 190 195	
gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca	739
Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro	
200 205 210	
gaa cta tgc gaa gcc cta gac att ccg atg tcc atg ctc cct gag att	787
Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile	
215 220 225	
cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta	835
Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg His Arg Gly Thr Leu	
230 235 240 245	
gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt	883
Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu	
250 255 260	
ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc	931
Phe Gly Gln Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
265 270 275	
acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
280 285 290	
gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct	1027
Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
295 300 305	
ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg	1075
Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
310 315 320 325	
cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att	1123
Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
330 335 340	
gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc	1171
Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val	
345 350 355	
cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt	1219
Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
360 365 370	

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
 1 5 10 15
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
 20 25 30
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
 35 40 45
 Pro Ser Lys Val Ser Asp Gln Lys Arg
 50 55

<210> 185
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1627)
 <223> RXA02640

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 aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115
 Met Arg Ile Ser Lys
 1 5
 gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163
 Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
 10 15 20
 tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211
 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
 25 30 35
 gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259
 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
 40 45 50
 gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307
 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
 55 60 65
 tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
 70 75 80 85
 cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
 Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
 90 95 100
 tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
 105 110 115
 gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc 499
 Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly
 120 125 130

290 295 300

Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
305 310 315 320

Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
325 330 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu
340 345 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg
355 360 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala
370 375 380

His Gly Ile Ser Gly His Met Ile Asn Phe
385 390

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<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXS01261

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atgcacgaca atgaccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115
Val Thr Glu His Tyr
1 5
gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163
Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
10 15 20
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
25 30 35
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
40 45 50
gat caa aaa cgc tgaagttgcc cataccttta ccc 294
Asp Gln Lys Arg
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<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 184

<210> 182
 <211> 394
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 <213> Corynebacterium glutamicum

<400> 182

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Asp	Lys	Ile	Val	Gly	Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	Lys	Ile
			20					25					30		
Ile	Glu	Ile	His	Gly	Leu	Gly	Asn	Phe	Lys	Asp	Ala	Lys	Thr	Leu	Glu
		35					40					45			
Val	Thr	Asp	Gly	Lys	Asp	Ala	Gly	Lys	Thr	Ile	Thr	Phe	Asp	Asp	Cys
	50					55					60				
Ile	Ile	Ala	Thr	Gly	Ser	Val	Val	Asn	Thr	Leu	Arg	Gly	Val	Asp	Phe
65					70					75					80
Ser	Glu	Asn	Val	Val	Ser	Phe	Glu	Glu	Gln	Ile	Leu	Asn	Pro	Val	Ala
			85						90					95	
Pro	Lys	Lys	Met	Val	Ile	Val	Gly	Ala	Gly	Ala	Ile	Gly	Met	Glu	Phe
			100					105					110		
Ala	Tyr	Val	Leu	Gly	Asn	Tyr	Gly	Val	Asp	Val	Thr	Val	Ile	Glu	Phe
		115					120					125			
Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Ala	Glu	Val	Ser	Lys	Val	Ile
	130					135					140				
Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala
145					150					155					160
Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln
			165						170					175	
Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met
			180					185					190		
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
		195					200					205			
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
	210					215					220				
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225				230						235				240	
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
			245						250					255	
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
		260						265					270		
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
		275					280					285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val

gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa 643
 Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys
 170 175 180

gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag 691
 Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys
 185 190 195

gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa 739
 Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln
 200 205 210

caa gct ggc gtt gat tac gcc act gtt agc gat ccc tct cgt ttc ctc 787
 Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp Pro Ser Arg Phe Leu
 215 220 225

gcg ccc tcc cct gct ggg gag ttg cac tgg taaataatct agtgaccaga 837
 Ala Pro Ser Pro Ala Gly Glu Leu His Trp
 230 235

ctg 840

<210> 204

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu
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His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp
 20 25 30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
 35 40 45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
 50 55 60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
 65 70 75 80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
 85 90 95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
 100 105 110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
 115 120 125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
 130 135 140

Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
 145 150 155 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile

Glu Lys Gln Gln Arg Gln Arg Gly Leu
245

<210> 203
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(817)
<223> RXN01580

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Met Tyr Lys Asn Met
1 5
cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr
10 15 20
atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp
25 30 35
atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc 259
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr
40 45 50
gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt 307
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val
55 60 65
gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga 355
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly
70 75 80 85
tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg 403
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro
90 95 100
atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca 451
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala
105 110 115
tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt 499
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser
120 125 130
ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct 547
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala
135 140 145
cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt 595
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu
150 155 160 165

gcc tgc gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723
 Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys
 225 230 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctacgcgacta 773
 Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu
 240 245

cac 776

<210> 202

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp
 20 25 30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly
 35 40 45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu
 50 55 60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe
 65 70 75 80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser
 85 90 95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro
 100 105 110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe
 115 120 125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp
 130 135 140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile
 145 150 155 160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp
 165 170 175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly
 180 185 190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly
 195 200 205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala
 210 215 220

Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu
 225 230 235 240

<221> CDS
 <222> (7)..(753)
 <223> RXA02414

<400> 201

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ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc 99
Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
                20             25             30

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147
Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
                35             40             45

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195
Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
                50             55             60

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
                65             70             75

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
                80             85             90             95

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339
Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
                100             105             110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387
Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
                115             120             125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435
Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
                130             135             140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483
Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
                145             150             155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531
Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
                160             165             170             175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579
Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
                180             185             190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627
Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
                195             200             205

ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675
Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
                210             215             220

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Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
 1 5 10 15
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala
 65 70 75 80
 Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser
 85 90 95
 Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
 100 105 110
 Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp
 115 120 125
 Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro
 130 135 140
 Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg
 145 150 155 160
 Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn
 165 170 175
 Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp
 180 185 190
 Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala
 195 200 205
 Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn
 210 215 220
 Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu
 225 230 235 240
 Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu
 245 250 255
 Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu
 260 265 270

Ile

<210> 201

<211> 776

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser				
	85	90	95	
acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc				336
Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile				
	100	105	110	
cag tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac				384
Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ser Phe Asp				
	115	120	125	
tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca				432
Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro				
	130	135	140	
acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt				480
Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg				
	145	150	155	160
cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac				528
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn				
	165	170	175	
act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat				576
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp				
	180	185	190	
gct gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca				624
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala				
	195	200	205	
tac aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac				672
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn				
	210	215	220	
ttc cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg				720
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu				
	225	230	235	240
gag aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag				768
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu				
	245	250	255	
gtt gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt				816
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu				
	260	265	270	
att taatccgagc acttcagcta cac				842
Ile				

<210> 200

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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 165 170 175
 Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr
 180 185 190
 Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala
 195 200 205
 Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr
 210 215 220
 Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe
 225 230 235 240
 Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu
 245 250 255
 Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val
 260 265 270
 Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile
 275 280 285

<210> 199
 <211> 842
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(819)
 <223> FRXA01891

<400> 199
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 Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
 1 5 10 15
 cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa 96
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac 192
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca 240
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala

180	185	190	
ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat gct			624
Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala			
195	200	205	
gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca tac			672
Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr			
210	215	220	
aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac ttc			720
Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe			
225	230	235	240
cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg gag			768
Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu			
245	250	255	
aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag gtt			816
Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val			
260	265	270	
gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt att			864
Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile			
275	280	285	
taatccgagc acttcagcta cac			887

<210> 198

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr		
1	5	10

Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro		
20	25	30

Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala		
35	40	45

Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu		
50	55	60

Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser		
65	70	75

Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val		
85	90	95

Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr		
100	105	110

Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln		
115	120	125

Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp		
130	135	140

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
275 280

<210> 197

<211> 887

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(864)

<223> RXN01891

<400> 197

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Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
1 5 10 15

tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca 96
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
20 25 30

gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
35 40 45

atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
50 55 60

tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct 240
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
65 70 75 80

gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt 288
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
85 90 95

gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc 336
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
100 105 110

gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag 384
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
115 120 125

tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac tgg 432
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
130 135 140

ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc 480
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145 150 155 160

ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag 528
Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
165 170 175

gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac act 576
Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr

Thr Glu Glu Asp Phe
280

<210> 196

<211> 282

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 196

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
1 5 10 15

Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
245 250 255

Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
260 265 270

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac	259
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp	
40 45 50	
aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg	307
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser	
55 60 65	
atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt	355
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val	
70 75 80 85	
aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct	403
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala	
90 95 100	
gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag	451
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys	
105 110 115	
ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca	499
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr	
120 125 130	
atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att	547
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile	
135 140 145	
gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag	595
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys	
150 155 160 165	
gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt	643
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val	
170 175 180	
tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat	691
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His	
185 190 195	
cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt	739
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly	
200 205 210	
agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt	787
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly	
215 220 225	
gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat	835
Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp	
230 235 240 245	
cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg	883
Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala	
250 255 260	
cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca	931
Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro	
265 270 275	
acg gaa gag gat ttt taagatggct ttggttcttg gaa	969

<210> 195
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

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<220>  
<221> CDS  
<222> (101)..(946)  
<223> RXA02288
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agtgcctggat ctaacaacat ttccgtggta actttttcac   atg tcc caa gtg att    115
                                     Met Ser Gln Val Ile
                                      1                      5

ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc    163
Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val
                        10                          15                  20

acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag    211
Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu
                    25                          30                  35
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agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt 499
 Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
 120 125 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
 Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
 135 140 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
 Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
 150 155 160 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
 Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
 170 175 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
 Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
 185 190 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739
 Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
 200 205 210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787
 Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
 215 220 225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
 230 235 240 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
 Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
 250 255

tgattcttac agtcactgca agt 900

<210> 194
 <211> 259
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 194
 Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val
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Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
 20 25 30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
 35 40 45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
 50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
 65 70 75 80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly

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<211> 900
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(877)  
<223> RXA01242
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gacatat																	115
gag																	5
Met Tyr Ala Glu Glu																	
1																	
cg	cgt	cga	cag	att	gcc	tca	tta	acg	gca	gtt	gag	gga	cgt	gta	aat		163
Arg	Arg	Arg	Gln	Ile	Ala	Ser	Leu	Thr	Ala	Val	Glu	Gly	Arg	Val	Asn		
10								15				20					
gtc	aca	gaa	tta	gcg	ggc	cga	ttc	gat	gtc	act	gca	gag	acg	att	cga		211
Val	Thr	Glu	Leu	Ala	Gly	Arg	Phe	Asp	Val	Thr	Ala	Glu	Thr	Ile	Arg		
25								30				35					
cga	gac	ctt	gcg	gtg	cta	gac	cgc	gag	gga	att	gtt	cac	cgc	gtt	cac		259
Arg	Asp	Leu	Ala	Val	Leu	Asp	Arg	Glu	Gly	Ile	Val	His	Arg	Val	His		
40								45				50					
ggt	ggc	gca	gta	gcc	acc	caa	tct	ttc	caa	acc	aca	gag	ttg	agc	ttg		307
Gly	Gly	Ala	Val	Ala	Thr	Gln	Ser	Phe	Gln	Thr	Thr	Glu	Leu	Ser	Leu		
55								60				65					
gat	act	cgt	ttc	agg	tct	gca	tcg	tca	gca	aag	tac	tcc	att	gcc	aag		355
Asp	Thr	Arg	Phe	Arg	Ser	Ala	Ser	Ser	Ala	Lys	Tyr	Ser	Ile	Ala	Lys		
70								75				80				85	
gca	gcg	atg	cag	ttc	ctg	ccc	gct	gag	cat	ggc	gga	ctg	ttc	ctc	gat		403
Ala	Ala	Met	Gln	Phe	Leu	Pro	Ala	Glu	His	Gly	Gly	Leu	Phe	Leu	Asp		
				90								95				100	
gcg	gga	act	act	gtt	act	gct	ttg	gcc	gat	ctc	att	tct	gag	cat	cct		451
Ala	Gly	Thr	Thr	Val	Thr	Ala	Leu	Ala	Asp	Leu	Ile	Ser	Glu	His	Pro		
				105				110				115					

His Ala Glu Arg Leu Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp
 180 185 190
 Gly Gly Thr Ala Ile Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn
 195 200 205
 Val Glu Glu Gly Arg Val Lys Gly Val Glu Val Thr Asp Gln Val Thr
 210 215 220
 Asn Thr Thr His Glu Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly
 225 230 235 240
 Pro Trp Val Ala Gln Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu
 245 250 255
 Lys Val Arg Gln Ser Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly
 260 265 270
 Ser Gln Ser Gly Val Phe Val Arg Gly Lys Asn Gly Lys His Val Ile
 275 280 285
 Val Asn Pro Trp Met Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met
 290 295 300
 Ile Asp Gly Asp Ala Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp
 305 310 315 320
 Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg
 325 330 335
 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp
 340 345 350
 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His
 355 360 365
 Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp
 370 375 380
 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu
 385 390 395 400
 His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln
 405 410 415
 Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser
 420 425 430
 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu
 435 440 445
 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val
 450 455 460
 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro
 465 470 475 480
 Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu
 485 490 495

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603
 Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu
 490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651
 Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val
 505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699
 Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr
 520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747
 Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala
 535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796
 Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg
 550 555 560

tcacgcgacac cgg 1809

<210> 192

<211> 562

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Met Thr Ser Ala His Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg
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Asp Asn Tyr Asp Val Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln
 20 25 30

Ile Ala Arg His Ala Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu
 35 40 45

Ala Arg Asp Tyr Ser Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile
 50 55 60

His Gly Gly Leu Arg Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln
 65 70 75 80

Glu Ala Val Lys Glu Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu
 85 90 95

Val Ala Pro Arg Ser Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro
 100 105 110

Lys Ala Pro Met Leu Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala
 115 120 125

Trp Gln Arg Asn Gln Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe
 130 135 140

Arg Trp Ile Pro Lys Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp
 145 150 155 160

Pro Glu Gly Leu Lys Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu
 165 170 175

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

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 <222> (101)..(1618)
 <223> RXA02539

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 Met Thr Val Tyr Ala
 1 5

aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag 163
 Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu
 10 15 20

aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt 211
 Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu
 25 30 35

gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt 259
 Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg
 40 45 50

ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc 307
 Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala
 55 60 65

gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg 355
 Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu
 70 75 80 85

cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt 403
 His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val
 90 95 100

gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca 451
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taatgccaac agcaagccca att

1140

<210> 216

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
100 105 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
115 120 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
130 135 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
145 150 155 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
165 170 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
180 185 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
195 200 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
210 215 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
245 250 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
260 265 270

90						95						100						
gca	ggt	gat	cct	gtg	cat	tgc	aga	gag	cgg	aag	att	cct	ggc	gtt	tct	451		
Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys	Ile	Pro	Gly	Val	Ser			
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tat	gcg	ggt	ggt	tggt	gca	cag	aat	att	gtt	gtt	cca	gcg	gag	gct	ctt	499		
Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val	Pro	Ala	Glu	Ala	Leu			
			120				125						130					
gct	gcg	att	cca	gat	ggc	atg	gac	ttt	tac	gag	ccc	gcc	ccg	atg	ggc	547		
Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu	Pro	Ala	Pro	Met	Gly			
			135				140				145							
tgc	gca	ggt	gtg	aca	aca	ttc	aat	gcg	ttg	cga	aac	ctg	aag	ctg	gat	595		
Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg	Asn	Leu	Lys	Leu	Asp			
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ccc	ggt	gcg	gct	gtc	gcg	gtc	ttt	gga	atc	ggc	ggt	tta	gtg	cgc	cta	643		
Pro	Gly	Ala	Ala	Val	Ala	Val	Phe	Gly	Ile	Gly	Gly	Leu	Val	Arg	Leu			
			170						175			180						
gct	att	cag	ttt	gct	gcg	aaa	atg	ggt	tat	cga	acc	atc	acc	atc	gcc	691		
Ala	Ile	Gln	Phe	Ala	Ala	Lys	Met	Gly	Tyr	Arg	Thr	Ile	Thr	Ile	Ala			
			185			190						195						
cgc	ggt	tta	gag	cgt	gag	gag	cta	gct	agg	caa	ctt	ggc	gcc	aac	cac	739		
Arg	Gly	Leu	Glu	Arg	Glu	Glu	Leu	Ala	Arg	Gln	Leu	Gly	Ala	Asn	His			
			200			205						210						
tac	atc	gat	agc	aat	gat	ctg	cac	cct	ggc	cag	gcg	tta	ttt	gaa	ctt	787		
Tyr	Ile	Asp	Ser	Asn	Asp	Leu	His	Pro	Gly	Gln	Ala	Leu	Phe	Glu	Leu			
			215			220						225						
ggc	ggg	gct	gac	ttg	atc	ttg	tct	act	gcg	tcc	acc	acg	gag	cct	ctt	835		
Gly	Gly	Ala	Asp	Leu	Ile	Leu	Ser	Thr	Ala	Ser	Thr	Thr	Glu	Pro	Leu			
230			235			240						245						
tcg	gag	ttg	tct	acc	ggt	ctt	tct	att	ggc	ggg	cag	cta	acc	att	atc	883		
Ser	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Ile	Gly	Gly	Gln	Leu	Thr	Ile	Ile			
			250			255						260						
gga	gtt	gat	ggg	gga	gat	atc	acc	gtt	tcg	gca	gcc	caa	ttg	atg	atg	931		
Gly	Val	Asp	Gly	Gly	Asp	Ile	Thr	Val	Ser	Ala	Ala	Gln	Leu	Met	Met			
			265			270						275						
aac	cgt	cag	atc	atc	aca	ggt	cac	ctc	act	gga	agt	gcg	aat	gac	acg	979		
Asn	Arg	Gln	Ile	Ile	Thr	Gly	His	Leu	Thr	Gly	Ser	Ala	Asn	Asp	Thr			
			280			285						290						
gaa	cag	act	atg	aaa	ttt	gct	cat	ctc	cat	ggc	gtg	aaa	ccg	ctt	att	1027		
Glu	Gln	Thr	Met	Lys	Phe	Ala	His	Leu	His	Gly	Val	Lys	Pro	Leu	Ile			
			295			300						305						
gaa	cgg	atg	cct	ctc	gat	caa	gcc	aac	gag	gct	att	gca	cgt	att	tca	1075		
Glu	Arg	Met	Pro	Leu	Asp	Gln	Ala	Asn	Glu	Ala	Ile	Ala	Arg	Ile	Ser			
310			315			320						325						
gct	ggt	aaa	cca	cgt	ttc	cgt	att	gtc	ttg	gag	ccg	aat	tca					

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
 65 70 75 80
 Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
 85 90 95
 Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
 100 105 110
 Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
 115 120 125
 Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
 130 135 140
 Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
 145 150 155 160
 Val Glu Ala Val

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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1117)
 <223> RXA01758

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 Met Pro Lys Tyr Ile 5
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val 20
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala 35
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys 50
 cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307
 His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile 65
 gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt 355
 Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val 85
 gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt 403
 Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg

gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc 163
 Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg
 10 15 20

aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act 211
 Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr
 25 30 35

tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc 259
 Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile
 40 45 50

ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt 307
 Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu
 55 60 65

ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag 355
 Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
 70 75 80 85

cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
 90 95 100

gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
 105 110 115

tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
 120 125 130

gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
 135 140 145

cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
 150 155 160

taggtttact gaagttcaga ctt 615

<210> 214

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
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Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
 20 25 30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
 35 40 45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
 50 55 60

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

Val Ser Ile Ser Val Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro
 1 5 10 15

Phe Glu Val Lys Ile Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val
 20 25 30

Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr
 35 40 45

Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His
 50 55 60

Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp
 65 70 75 80

Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly
 85 90 95

Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly
 100 105 110

Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln
 115 120 125

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
 165 170 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
 180 185 190

Pro Asp Arg Cys Ser Gln Gly Cys
 195 200

<210> 213

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA01572

<400> 213

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gacaaagtag cagtcattggg cctcggcggg actcggacac atg ggt gtc cag atc 115
 Met Gly Val Gln Ile
 1 5

$$\begin{array}{ll} \langle 210 \rangle & 212 \\ \langle 211 \rangle & 200 \end{array}$$

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr
 100 105 110
 Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe
 115 120 125
 Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp
 130 135 140
 Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr
 145 150 155 160
 Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met
 165 170 175
 Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala
 180 185 190
 Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys
 195 200 205
 Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg
 210 215 220
 Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala
 225 230 235 240
 His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala
 245 250 255
 Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro
 260 265 270
 Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu
 275 280 285
 Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala
 290 295 300
 Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys
 305 310 315 320
 Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys
 325 330 335
 Ile Asp Gly Arg Val Ala Ile Arg Phe
 340 345

<210> 211
 <211> 723
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(700)
 <223> RXA01571

<400> 211

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 Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly
 215 220 225
 gaa gct gta cag aag tac acc aac ggt ggc gca cac ggc gtg ctt gtg 835
 Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala His Gly Val Leu Val
 230 235 240 245
 act gca gtt cac gag gca gca ttc ggc cag gca ctg gat atg gct cga 883
 Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala Leu Asp Met Ala Arg
 250 255 260
 cgt gca gga aca att gtg ttc aac ggt ctg cca ccg gga gag ttc cca 931
 Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro
 265 270 275
 gca tcc gtg ttc aac atc gta ttc aag ggc ctg acc atc cgt gga tcc 979
 Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu Thr Ile Arg Gly Ser
 280 285 290
 ctc gtg gga acc cgc caa gac ttg gcc gaa gcg ctc gat ttc ttt gca 1027
 Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala Leu Asp Phe Phe Ala
 295 300 305
 cgc gga cta atc aag cca acc gtg agt gag tgc tcc ctc gat gag gtc 1075
 Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val
 310 315 320 325
 aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123
 Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val
 330 335 340
 gcg att cgt ttc taacggattg tgttgaaact gct 1158
 Ala Ile Arg Phe
 345

<210> 210

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

Met Thr Thr Ala Ala Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys
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Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly
 20 25 30

Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr
 35 40 45

Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro
 50 55 60

Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro
 65 70 75 80

Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu
 85 90 95

<222> (101)..(1135)

<223> RXA00246

<400> 209

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gcaatttgcc aagtaatcca agcgagaagg agtgagtttt atg acc act gct gca 115
 Met Thr Thr Ala Ala
 1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163
 Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val
 10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211
 Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu
 25 30 35

gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259
 Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu
 40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307
 Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His
 55 60 65

gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355
 Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val
 70 75 80 85

aag gtc ggc gat att gtc ggc aat gcg tgg ctc tgg tca gcg tgt ggc 403
 Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu Trp Ser Ala Cys Gly
 90 95 100

acc tgc gaa tac tgc atc acc ggc agg gaa act cag tgc aac gaa gct 451
 Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr Gln Cys Asn Glu Ala
 105 110 115

gag tat ggt ggc tac acc caa aat gga tcc ttc ggc cag tac atg ctg 499
 Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe Gly Gln Tyr Met Leu
 120 125 130

gtg gat acc cgt tac gcc gct cgc atc cca gac ggc gtg gac tac ctc 547
 Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp Gly Val Asp Tyr Leu
 135 140 145

gaa gca gca cca att ctg tgt gca ggc gtg act gtc tac aag gca ctc 595
 Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu
 150 155 160 165

aaa gtc tct gaa acc cgc ccg ggc caa ttc atg gtg atc tcc ggt gtc 643
 Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met Val Ile Ser Gly Val
 170 175 180

ggc gga ctt ggc cac atc gca gtc caa tac gca gcg gcg atg ggc atg 691
 Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala Ala Ala Met Gly Met
 185 190 195

cgt gtc att gcg gta gat att gcc gat gac aag ctg gaa ctt gcc cgt 739
 Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg
 200 205 210

<400> 208

Met Ala Gly Gly Asn Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val
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Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
 20 25 30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
 35 40 45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
 50 55 60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
 65 70 75 80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
 85 90 95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
 100 105 110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
 115 120 125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
 130 135 140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
 145 150 155 160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
 165 170 175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
 180 185 190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
 195 200 205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
 210 215 220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
 225 230 235 240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
 245 250 255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
 260 265

<210> 209

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
    55                      60                      65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355
Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
    70                      75                      80                      85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403
Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu
                      90                      95                      100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac 451
Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
    105                      110                      115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt 499
Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
    120                      125                      130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547
Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
    135                      140                      145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc 595
Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
    150                      155                      160                      165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643
Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
                      170                      175                      180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga 691
Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
    185                      190                      195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739
Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
    200                      205                      210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt 787
Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu
    215                      220                      225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa 835
Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
    230                      235                      240                      245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883
Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
    250                      255                      260

gca gaa cga aaa ggc gat acc taaacccgcc ctccatctgc ata 927
Ala Glu Arg Lys Gly Asp Thr
    265

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<210> 208

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

Thr Arg Ser Gly Asp Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg
 245 250 255

Thr Ala Gly Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys
 260 265 270

Ser Gly Val Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg
 275 280 285

Glu Met Ile Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile
 290 295 300

Tyr Ile His Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu
 305 310 315 320

Gly Arg Val Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala
 325 330 335

Gln Phe Val Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile
 340 345 350

Glu Ile Asp Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu
 355 360 365

Ile Ser Thr Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn
 370 375 380

Glu Glu Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
 385 390 395

<210> 207

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA00686

<400> 207

ataggcttga acaatacgtc gttacactgg ccgatttgat acctttcaaa acttttaccc 60

ttcatcggag tgccagggga acttagagga gcattaaata atg gcg gga gga aat 115
 Met Ala Gly Gly Asn
 1 5

cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163
 Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
 10 15 20

gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag 211
 Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
 25 30 35

ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta 259
 Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
 40 45 50

360 365 370

tcc aag gtg aag gtg ttt gtt att cca act aat gaa gag tta gct atc 1267
 Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile
 375 380 385

gct agg tac gcg gtg aag ttc gct tagctctcct ggtaggatac cac 1314
 Ala Arg Tyr Ala Val Lys Phe Ala
 390 395

<210> 206

<211> 397

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Met Ala Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe
 1 5 10 15

Gln Leu Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser
 20 25 30

Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys
 35 40 45

Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser
 50 55 60

Glu Gly Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly
 65 70 75 80

Pro Ser Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly
 85 90 95

Gly Ile Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu
 100 105 110

Met Ile Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn
 115 120 125

Val Asp Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His
 130 135 140

Val Ala Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala
 145 150 155 160

Ala Leu Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg
 165 170 175

Arg Tyr Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val
 180 185 190

Val Glu Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe
 195 200 205

His Leu Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala
 210 215 220

Val Asp Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly
 225 230 235 240

Ile	Pro	Leu	Ala	Pro	Leu	His	Asn	Pro	Ala	Asn	Val	Asp	Gly	Ile	Asp		
		120					125					130					
gtt	gct	cga	aaa	att	ctc	ccc	gat	gtc	cca	cac	gta	gct	gtc	ttt	gac	547	
Val	Ala	Arg	Lys	Ile	Leu	Pro	Asp	Val	Pro	His	Val	Ala	Val	Phe	Asp		
		135				140					145						
acc	ggt	ttc	ttc	cac	tca	ctt	cca	cca	gca	gct	gcg	ctg	tat	gcc	atc	595	
Thr	Gly	Phe	Phe	His	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Leu	Tyr	Ala	Ile		
		150			155					160					165		
aac	aag	gat	gtc	gca	gct	gaa	cac	gga	atc	agg	cgc	tat	ggt	ttc	cac	643	
Asn	Lys	Asp	Val	Ala	Ala	Glu	His	Gly	Ile	Arg	Arg	Tyr	Gly	Phe	His		
				170					175						180		
ggc	acc	tcc	cat	gaa	ttt	gtg	tcc	aag	cgc	gtg	gtg	gaa	att	ctg	gaa	691	
Gly	Thr	Ser	His	Glu	Phe	Val	Ser	Lys	Arg	Val	Val	Glu	Ile	Leu	Glu		
			185					190					195				
aag	ccc	acc	gaa	gac	atc	aac	acc	atc	acc	ttc	cac	ctg	ggc	aac	ggc	739	
Lys	Pro	Thr	Glu	Asp	Ile	Asn	Thr	Ile	Thr	Phe	His	Leu	Gly	Asn	Gly		
		200					205					210					
gca	tcc	atg	gct	gct	gtt	caa	ggt	ggc	cgt	gcg	gta	gat	act	tcc	atg	787	
Ala	Ser	Met	Ala	Ala	Val	Gln	Gly	Gly	Arg	Ala	Val	Asp	Thr	Ser	Met		
		215				220					225						
ggt	atg	aca	cct	ctc	gcg	ggc	ctt	gtc	atg	ggt	acc	cga	agc	ggt	gac	835	
Gly	Met	Thr	Pro	Leu	Ala	Gly	Leu	Val	Met	Gly	Thr	Arg	Ser	Gly	Asp		
		230			235					240					245		
att	gat	cca	ggt	atc	gtc	ttc	cac	ctt	tcc	cgc	acc	gct	ggc	atg	agc	883	
Ile	Asp	Pro	Gly	Ile	Val	Phe	His	Leu	Ser	Arg	Thr	Ala	Gly	Met	Ser		
				250					255						260		
atc	gat	gag	atc	gat	aat	ctg	ctg	aac	aaa	aag	tcg	ggt	gta	aag	gga	931	
Ile	Asp	Glu	Ile	Asp	Asn	Leu	Leu	Asn	Lys	Lys	Ser	Gly	Val	Lys	Gly		
			265					270					275				
ctt	tcc	ggt	gtt	aat	gat	ttc	cgt	gaa	ctg	cgg	gaa	atg	atc	gac	aac	979	
Leu	Ser	Gly	Val	Asn	Asp	Phe	Arg	Glu	Leu	Arg	Glu	Met	Ile	Asp	Asn		
		280					285					290					
aat	gat	caa	gat	gcc	tgg	tcc	gcg	tac	aac	att	tac	ata	cac	caa	ctc	1027	
Asn	Asp	Gln	Asp	Ala	Trp	Ser	Ala	Tyr	Asn	Ile	Tyr	Ile	His	Gln	Leu		
		295				300					305						
cgc	cgc	tac	ctc	ggt	tcc	tac	atg	gtg	gca	ctg	gga	cgg	gta	gac	acc	1075	
Arg	Arg	Tyr	Leu	Gly	Ser	Tyr	Met	Val	Ala	Leu	Gly	Arg	Val	Asp	Thr		
		310			315					320					325		
atc	gtg	ttc	acc	gcc	ggt	gtc	ggt	gaa	aat	gcc	cag	ttt	gtc	cgt	gag	1123	
Ile	Val	Phe	Thr	Ala	Gly	Val	Gly	Glu	Asn	Ala	Gln	Phe	Val	Arg	Glu		
				330					335						340		
gat	gcc	ttg	gca	ggt	ttg	gaa	atg	tac	gga	att	gag	atc	gat	cca	gag	1171	
Asp	Ala	Leu	Ala	Gly	Leu	Glu	Met	Tyr	Gly	Ile	Glu	Ile	Asp	Pro	Glu		
			345					350					355				
cgt	aac	gca	ttg	cca	aac	gat	ggt	cct	cga	ttg	att	tcc	acc	gat	gcc	1219	
Arg	Asn	Ala	Leu	Pro	Asn	Asp	Gly	Pro	Arg	Leu	Ile	Ser	Thr	Asp	Ala		

[illegible]

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1663)

<223> RXN01498

<400> 225

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accacacgag catcagaacg cgaaacgaag gtaaaagccc atg atc aaa cgt ctt 115
 Met Ile Lys Arg Leu
 1 5

cct tta ggt ccg ctg cct aaa gaa ctt cat cag act ctg ctt gat ctg 163
 Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln Thr Leu Leu Asp Leu
 10 15 20

acc gca aat gcc caa gat gcg gcg aaa gtg gag gtt ata gcg cca ttt 211
 Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu Val Ile Ala Pro Phe
 25 30 35

act ggc gag acc ctc gga ttt ggt ttt gat ggt gat gag caa gac gtc 259
 Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly Asp Glu Gln Asp Val
 40 45 50

gag cat gct ttt gca ctt tca agg gca gcc cag aaa aag tgg gtg cac 307
 Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln Lys Lys Trp Val His
 55 60 65

acc acg gca gtg gaa cgg aag aag atc ttc ctg aag gtt cat gat ctg 355
 Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu Lys Val His Asp Leu
 70 75 80 85

gta ttg aaa aac cgt gag ctg ctc atg gac atc gtg cag ttg gaa aca 403
 Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile Val Gln Leu Glu Thr
 90 95 100

ggc aaa aat cga gca tcg gct gcc gat gag gtg ttg gac gtt gcg atc 451
 Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val Leu Asp Val Ala Ile
 105 110 115

acc acc cgc ttc tac gca aac aat gca gga aag ttt tta aat gac aag 499
 Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys Phe Leu Asn Asp Lys
 120 125 130

aaa cgc ccc ggc gcg ctt ccg atc atc acg aaa aac aca caa cag tat 547
 Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys Asn Thr Gln Gln Tyr
 135 140 145

gtg ccc aag gga gtg gtc ggg cag atc acg ccg tgg aat tac cct tta 595
 Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro Trp Asn Tyr Pro Leu
 150 155 160 165

act ttg gga gta tct gat gct gtt ccg gcg ctg ctg gca gga aac gca 643
 Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu Leu Ala Gly Asn Ala
 170 175 180

gtg gtg gct aaa cct gac ctc gcg aca cct ttc tcc tgc ttg atc atg 691
 Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe Ser Cys Leu Ile Met
 185 190 195

<213> Corynebacterium glutamicum

<400> 224

Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15

Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30

Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45

Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
 65 70 75 80

Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
 85 90 95

Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
 100 105 110

His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
 115 120 125

Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
 130 135 140

Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
 145 150 155 160

Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
 165 170 175

Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
 180 185 190

Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
 195 200 205

Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
 210 215 220

Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
 225 230 235 240

Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
 245 250 255

Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
 260 265 270

Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
 275 280 285

<210> 225

<211> 1686

<212> DNA

Leu	Arg	Thr	Ser	Met	Glu	Leu	Gly	Gly	Asn	Ala	Ala	Phe	Val	Ile	Asp	
65					70					75					80	
gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa 288																
Glu	Ala	Ala	Asp	Leu	Asp	Glu	Ala	Val	Ser	Gly	Ala	Ile	Ala	Ala	Lys	
				85					90					95		
ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt 336																
Leu	Arg	Asn	Ala	Gly	Gln	Val	Cys	Ile	Ala	Ala	Asn	Arg	Phe	Leu	Val	
			100					105					110			
cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg 384																
His	Glu	Ser	Arg	Ala	Ala	Glu	Phe	Thr	Ser	Lys	Leu	Ala	Thr	Ala	Met	
		115					120					125				
cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg 432																
Gln	Asn	Thr	Pro	Ile	Gly	Pro	Val	Ile	Ser	Ala	Arg	Gln	Arg	Asp	Arg	
	130					135					140					
atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc 480																
Ile	Ala	Ala	Leu	Val	Asp	Glu	Ala	Ile	Thr	Asp	Gly	Ala	Arg	Leu	Ile	
145					150					155				160		
atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc 528																
Ile	Gly	Gly	Glu	Val	Pro	Asp	Gly	Ser	Gly	Phe	Phe	Tyr	Pro	Ala	Thr	
			165					170						175		
atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc 576																
Ile	Leu	Ala	Asp	Val	Pro	Ala	Gln	Ser	Arg	Ile	Val	His	Glu	Glu	Ile	
			180					185					190			
ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc 624																
Phe	Gly	Pro	Val	Ala	Thr	Ile	Ala	Thr	Phe	Thr	Asp	Leu	Ala	Glu	Gly	
		195					200					205				
gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc 672																
Val	Ala	Gln	Ala	Asn	Ser	Thr	Glu	Phe	Gly	Leu	Ala	Ala	Tyr	Gly	Phe	
	210					215					220					
agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc 720																
Ser	Asn	Asn	Val	Lys	Ala	Thr	Gln	Tyr	Met	Ala	Glu	His	Leu	Glu	Ala	
225					230					235				240		
gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct 768																
Gly	Met	Val	Gly	Ile	Asn	Arg	Gly	Ala	Ile	Ser	Asp	Pro	Ala	Ala	Pro	
				245				250					255			
ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa 816																
Phe	Gly	Gly	Ile	Gly	Gln	Ser	Gly	Phe	Gly	Arg	Glu	Gly	Gly	Thr	Glu	
			260					265					270			
gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg 858																
Gly	Ile	Glu	Glu	Tyr	Leu	Ser	Val	Arg	Tyr	Leu	Ala	Leu	Pro			
	275						280					285				
tgacacatga gctgtccggt gaa 881																

<210> 224

<211> 286

<212> PRT

50 55 60
 Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
 65 70 75 80
 Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
 85 90 95
 Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
 100 105 110
 Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
 115 120 125
 Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
 130 135 140
 Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
 145 150 155 160
 Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
 165 170 175
 Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
 180 185 190
 Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 195 200 205

<210> 223

<211> 881

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(858)

<223> RXN01340

<400> 223

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 Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15
 cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg 96
 Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30
 gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga 144
 Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45
 tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg 192
 Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60
 ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac 240

40	45	50	
cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc			307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser			
55	60	65	
tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc			355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly			
70	75	80	85
agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg			403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val			
90	95	100	
ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc			451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe			
105	110	115	
gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc			499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile			
120	125	130	
caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg			547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Thr Val Trp Thr			
135	140	145	
agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga			595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly			
150	155	160	165
acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga			643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly			
170	175	180	
ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt			691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu			
185	190	195	
gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata			744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu			
200	205		
tat			747

<210> 222

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Val	Glu	Ala	Gln	Phe	Thr	Ser	Pro	Leu	Leu	Asn	Asn	Gly	Gln	Thr	Cys
1				5					10					15	

Phe	Leu	Gly	Thr	Arg	Ile	Leu	Ala	Pro	Lys	Ser	Arg	Tyr	Ala	Glu	Val
			20					25					30		

Val	Asp	Ala	Phe	Thr	Ala	Phe	Ala	Gly	Ser	Leu	Gln	Val	Gly	Val	Thr
	35						40					45			

Ser	Ser	Pro	Asp	Thr	Gln	Ile	Gly	Pro	Met	Ala	Thr	Ala	Arg	Gln	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

405	410	415
Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala		
420	425	430
Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala		
435	440	445
Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala		
450	455	460
His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn		
465	470	475
His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val		
485	490	495
Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe		
500	505	

<210> 219
 <211> 430
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(430)
 <223> RXN03061

<400> 219
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 gccctagagc gcgaaaccgc gcaccagaag gtgggctaaa gtg tct ttg acc ttc 115
 Val Ser Leu Thr Phe
 1 5
 cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac 163
 Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn
 10 15 20
 cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct 211
 His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala
 25 30 35
 ggt cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc 259
 Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu
 40 45 50
 acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag 307
 Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu
 55 60 65
 atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa 355
 Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu
 70 75 80 85
 gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg 403
 Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val
 90 95 100

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
 85 90 95
 Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
 100 105 110
 Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
 115 120 125
 Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
 130 135 140
 His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
 145 150 155 160
 Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
 165 170 175
 Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
 180 185 190
 Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
 195 200 205
 Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
 210 215 220
 Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
 225 230 235 240
 Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
 245 250 255
 Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
 260 265 270
 Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
 275 280 285
 Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
 290 295 300
 Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
 305 310 315 320
 Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
 325 330 335
 Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
 340 345 350
 Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
 355 360 365
 Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
 370 375 380
 Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg
 385 390 395 400
 Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe

Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val
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<213> Corynebacterium glutamicum

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 Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
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 Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
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Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp	
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Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala	
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Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val	
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Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu	
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Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile Gly His Leu Ser Glu	
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Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala	
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Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile Ala Gly Gly Gly Val	
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Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys	
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His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val	
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 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe
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 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg
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 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala
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 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr
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 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser
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 Ile Gly Ala Gly Phe Glu Trp Lys Tyr Gly Met Gly Ser Leu Ile Asn
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 His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala
 340 345 350
 Ala Gly Ala Thr Val Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly
 355 360 365
 Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr
 370 375 380
 Pro Leu Leu Thr Glu Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys
 385 390 395 400
 Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr
 405 410 415
 Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val
 420 425 430
 Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala
 435 440 445
 Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser
 450 455 460
 Gly Leu Gly His Arg His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu
 465 470 475 480
 Ile Arg Asn Ile Ala Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala

gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc 1459
 Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser
 440 445 450

gtg tcc acg cct ctg ggt ggc atg aag cag tcg ggg ctg ggg cac cgc 1507
 Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg
 455 460 465

cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg 1555
 His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala
 470 475 480 485

gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag 1603
 Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys
 490 495 500

gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt 1651
 Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe
 505 510 515

aaa gtt ttg ccg tagcaaaaag ccggaccctt gct 1686
 Lys Val Leu Pro
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<210> 226

<211> 521

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

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Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly
 35 40 45

Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln
 50 55 60

Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu
 65 70 75 80

Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile
 85 90 95

Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val
 100 105 110

Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys
 115 120 125

Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys
 130 135 140

Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro
 145 150 155 160

gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt	739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val	
200 205 210	
gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt	787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys	
215 220 225	
gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt	835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly	
230 235 240 245	
cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga	883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly	
250 255 260	
aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa	931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu	
265 270 275	
gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc	979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val	
280 285 290	
tcc act gaa cgt att tat gtc gag gaa gac gtg tac gag gag gtg att	1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile	
295 300 305	
gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt	1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe	
310 315 320 325	
gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat	1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp	
330 335 340	
cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg	1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val	
345 350 355	
ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag	1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu	
360 365 370	
ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag	1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu	
375 380 385	
gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa	1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu	
390 395 400 405	
gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc	1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser	
410 415 420	
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa	1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu	
425 430 435	

Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
195 200 205

Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
210 215 220

Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
225 230 235 240

Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
245 250 255

Tyr Asn

<210> 239

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXA02453

<400> 239

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tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115
Met Lys Ser Ile Phe
1 5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163
Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
10 15 20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211
Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
25 30 35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259
Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
40 45 50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307
Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
55 60 65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355
Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
70 75 80 85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403
Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
90 95 100

gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451
Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
105 110 115

gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag 739
 Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu
 200 205 210

tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta 787
 Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val
 215 220 225

gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc 835
 Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr
 230 235 240 245

gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac taggggttgc 884
 Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn
 250 255

tttcccgac tca 897

<210> 238
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 238
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 Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
 20 25 30
 Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
 35 40 45
 Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
 50 55 60
 Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
 65 70 75 80
 Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
 85 90 95
 Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
 100 105 110
 Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
 115 120 125
 Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
 130 135 140
 Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
 145 150 155 160
 Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
 165 170 175
 His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
 180 185 190

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA02474

<400> 237

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				Met	Ser	Lys	Val	Ala	
				1				5	

atg	ggt	acc	ggt	ggt	gca	caa	ggc	atc	ggt	cgt	gga	att	tca	gag	aag	163
Met	Val	Thr	Gly	Gly	Ala	Gln	Gly	Ile	Gly	Arg	Gly	Ile	Ser	Glu	Lys	
			10					15						20		

ctg	gca	gca	gat	ggt	ttc	gat	att	gcc	gta	gcc	gac	ctg	cca	caa	cag	211
Leu	Ala	Ala	Asp	Gly	Phe	Asp	Ile	Ala	Val	Ala	Asp	Leu	Pro	Gln	Gln	
			25				30						35			

gaa	gaa	caa	gct	gca	gag	acc	atc	aag	ttg	att	gaa	gct	gca	ggt	caa	259
Glu	Glu	Gln	Ala	Ala	Glu	Thr	Ile	Lys	Leu	Ile	Glu	Ala	Ala	Gly	Gln	
		40					45				50					

aag	gct	gta	ttc	ggt	gga	tta	gat	gtc	acc	gat	aag	gct	aat	ttc	gac	307
Lys	Ala	Val	Phe	Val	Gly	Leu	Asp	Val	Thr	Asp	Lys	Ala	Asn	Phe	Asp	
	55					60					65					

agt	gca	att	gat	gag	gca	gca	gag	aaa	ctt	ggc	ggc	ttc	gat	gtg	cta	355
Ser	Ala	Ile	Asp	Glu	Ala	Ala	Glu	Lys	Leu	Gly	Gly	Phe	Asp	Val	Leu	
	70				75				80						85	

gta	aac	aac	gcc	ggc	atc	gca	caa	att	aag	cca	ctt	ctg	gaa	gtc	acc	403
Val	Asn	Asn	Ala	Gly	Ile	Ala	Gln	Ile	Lys	Pro	Leu	Leu	Glu	Val	Thr	
			90					95						100		

gaa	gaa	gac	cta	aag	cag	atc	tac	tcc	gtg	aac	ggt	ttt	agc	gta	ttt	451
Glu	Glu	Asp	Leu	Lys	Gln	Ile	Tyr	Ser	Val	Asn	Val	Phe	Ser	Val	Phe	
		105					110					115				

ttt	ggt	att	caa	gca	gca	tcc	cga	aag	ttc	gat	gag	ctt	ggc	gta	aaa	499
Phe	Gly	Ile	Gln	Ala	Ala	Ser	Arg	Lys	Phe	Asp	Glu	Leu	Gly	Val	Lys	
		120				125					130					

ggc	aag	atc	atc	aac	gct	gca	tca	atc	gct	gct	atc	caa	ggt	ttc	cca	547
Gly	Lys	Ile	Ile	Asn	Ala	Ala	Ser	Ile	Ala	Ala	Ile	Gln	Gly	Phe	Pro	
	135				140				145							

atc	ttg	agc	gcc	tac	tcc	acc	acc	aaa	ttc	gcg	ggt	cgt	ggc	ctc	acc	595
Ile	Leu	Ser	Ala	Tyr	Ser	Thr	Thr	Lys	Phe	Ala	Val	Arg	Gly	Leu	Thr	
	150				155				160					165		

cag	gct	gct	gcg	caa	gaa	ctc	gca	ccc	aag	ggt	cac	acc	gtg	aat	gcc	643
Gln	Ala	Ala	Ala	Gln	Glu	Leu	Ala	Pro	Lys	Gly	His	Thr	Val	Asn	Ala	
			170					175						180		

tac	gca	cct	ggc	atc	gtg	ggc	acc	gga	atg	tgg	gag	caa	atc	gat	gcc	691
Tyr	Ala	Pro	Gly	Ile	Val	Gly	Thr	Gly	Met	Trp	Glu	Gln	Ile	Asp	Ala	
		185				190							195			

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc 499
 Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr
 120 125 130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc 547
 Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile
 135 140 145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag 595
 Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys
 150 155 160 165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc 639
 Thr Met Ala Pro Ala Lys Ile
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<210> 236

<211> 172

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

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Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 20 25 30

Ala Phe Asn Leu Val Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly
 35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
 50 55 60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
 65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
 85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
 100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
 115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
 130 135 140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
 145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
 165 170

<210> 237

<211> 897

<212> DNA

Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp
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Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu
 180 185 190

Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val
 195 200 205

Gly Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe
 210 215 220

Ala Glu Tyr Thr Gly Ile Pro
 225 230

<210> 235

<211> 639

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(616)

<223> RXN01144

<400> 235

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gccgccgttg aatcgaccga ggcataagga gagacccaag atg gct aat tct gac 115
 Met Ala Asn Ser Asp
 1 5

gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc 163
 Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile
 10 15 20

att tcc cgc gta tca ggt atg ttc acc cga cgc gca ttc aac ctc gtg 211
 Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val
 25 30 35

ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg 259
 Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr
 40 45 50

gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag 307
 Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln
 55 60 65

ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag 355
 Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu
 70 75 80 85

acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc 403
 Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser
 90 95 100

acc aac cgt ccg cag atc gtc gac gcc gcg aac atc ttc cgc gcc cga 451
 Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn Ile Phe Arg Ala Arg
 105 110 115

cgc cct ggc cct gtt ctg gtg gat att cct aag gat gtc cag aac gct 595
 Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn Ala
 150 155 160 165
 gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac cgc 643
 Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr Arg
 170 175 180
 cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag ctg 691
 Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys Leu
 185 190 195
 atc ggt gag gcc aag aag ccc gtc ctt tac gtt ggt ggt ggc gta atc 739
 Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Val Ile
 200 205 210
 aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc ggc 787
 Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe Ala Glu Tyr Thr Gly
 215 220 225
 atc cca 793
 Ile Pro
 230

<210> 234
 <211> 231
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 234
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 Asp Ile Val Phe Gly Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp
 20 25 30
 Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu
 35 40 45
 Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg
 50 55 60
 Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 65 70 75 80
 Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
 85 90 95
 Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu
 100 105 110
 Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met
 115 120 125
 Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His
 130 135 140
 Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
 145 150 155 160

340 345 350
 Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
 355 360 365
 Glu Ser Thr Glu Ala
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 <222> (101)..(793)
 <223> RXN01146
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 Met Thr Gly Ala Lys
 1 5
 gca att gtt cga tcg ctc gag gag ctt aac gcc gac atc gtg ttc ggt 163
 Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala Asp Ile Val Phe Gly
 10 15 20
 att cct ggt ggt gcg gtg cta ccg gtg tat gac ccg ctc tat tcc tcc 211
 Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp Pro Leu Tyr Ser Ser
 25 30 35
 aca aag gtg cgc cac gtc ttg gtg cgc cac gag cag ggc gca ggc cac 259
 Thr Lys Val Arg His Val Leu Val Arg His Glu Gln Gly Ala Gly His
 40 45 50
 gca gca acc ggc tac gcg cag gtt act gga cgc gtt ggc gtc tgc att 307
 Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg Val Gly Val Cys Ile
 55 60 65
 gca acc tct ggc cca gga gca acc aac ttg gtt acc cca atc gct gat 355
 Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Pro Ile Ala Asp
 70 75 80 85
 gca aac ttg gac tcc gtt ccc atg gtt gcc atc acc ggc cag gtc gga 403
 Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile Thr Gly Gln Val Gly
 90 95 100
 agt ggc ctg ctg ggt acc gac gct ttc cag gaa gcc gat atc cgc ggc 451
 Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu Ala Asp Ile Arg Gly
 105 110 115
 atc acc atg cca gtg acc aag cac, aac ttc atg gtc acc aac cct aac 499
 Ile Thr Met Pro Val Thr Lys His Asn Phe Met Val Thr Asn Pro Asn
 120 125 130
 gac att cca cag gca ttg gct gag gca ttc cac ctc gcg att act ggt 547
 Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His Leu Ala Ile Thr Gly
 135 140 145

His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
 20 25 30
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
 50 55 60
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
 65 70 75 80
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
 85 90 95
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
 100 105 110
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
 115 120 125
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
 130 135 140
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
 145 150 155 160
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
 165 170 175
 Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
 180 185 190
 Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
 195 200 205
 Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
 210 215 220
 Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
 225 230 235 240
 Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
 245 250 255
 Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
 260 265 270
 Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
 275 280 285
 Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
 290 295 300
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
 305 310 315 320
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
 325 330 335
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu

Arg	Thr	Trp	Leu	Asn	Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Tyr	Ala	Val		
			180					185					190				
cct	gcg	gcc	ctt	gga	gca	aag	gct	ggc	gca	cct	gac	aag	gaa	gtc	tgg	624	
Pro	Ala	Ala	Leu	Gly	Ala	Lys	Ala	Gly	Ala	Pro	Asp	Lys	Glu	Val	Trp		
		195					200					205					
gct	atc	gac	ggc	gac	ggc	tgt	ttc	cag	atg	acc	aac	cag	gaa	ctc	acc	672	
Ala	Ile	Asp	Gly	Asp	Gly	Cys	Phe	Gln	Met	Thr	Asn	Gln	Glu	Leu	Thr		
	210					215					220						
acc	gcc	gca	gtt	gaa	ggc	ttc	ccc	att	aag	atc	gca	cta	atc	aac	aac	720	
Thr	Ala	Ala	Val	Glu	Gly	Phe	Pro	Ile	Lys	Ile	Ala	Leu	Ile	Asn	Asn		
225					230					235					240		
gga	aaa	cct	ggg	gca	tgg	gtt	cgc	caa	tgg	cag	acc	cta	ttc	tat	gaa	768	
Gly	Lys	Pro	Gly	Ala	Trp	Val	Arg	Gln	Trp	Gln	Thr	Leu	Phe	Tyr	Glu		
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gga	cgg	tac	tca	aat	act	aaa	ctt	cgt	aac	cag	ggc	gag	tac	atg	ccc	816	
Gly	Arg	Tyr	Ser	Asn	Thr	Lys	Leu	Arg	Asn	Gln	Gly	Glu	Tyr	Met	Pro		
			260					265					270				
gac	ttt	gtt	acc	ctt	tct	gag	gga	ctt	ggc	tgt	gtt	gcc	atc	cgc	gtc	864	
Asp	Phe	Val	Thr	Leu	Ser	Glu	Gly	Leu	Gly	Cys	Val	Ala	Ile	Arg	Val		
		275					280					285					
acc	aaa	gcg	gag	gaa	gta	ctg	cca	gcc	atc	caa	aag	gct	cga	gag	atc	912	
Thr	Lys	Ala	Glu	Glu	Val	Leu	Pro	Ala	Ile	Gln	Lys	Ala	Arg	Glu	Ile		
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aac	gac	cgc	cca	gta	gtc	atc	gac	ttc	atc	gtc	ggc	gaa	gac	gca	cag	960	
Asn	Asp	Arg	Pro	Val	Val	Ile	Asp	Phe	Ile	Val	Gly	Glu	Asp	Ala	Gln		
305					310					315					320		
gta	tgg	cca	atg	gtg	tct	gct	gga	tca	tcc	aac	tcc	gat	atc	cag	tac	1008	
Val	Trp	Pro	Met	Val	Ser	Ala	Gly	Ser	Ser	Asn	Ser	Asp	Ile	Gln	Tyr		
				325					330					335			
gca	ctc	gga	ttg	cgc	cca	ttc	ttt	gat	ggc	gat	gaa	tct	gca	gca	gaa	1056	
Ala	Leu	Gly	Leu	Arg	Pro	Phe	Phe	Asp	Gly	Asp	Glu	Ser	Ala	Ala	Glu		
			340					345					350				
gat	cct	gcc	gac	att	cac	gaa	gcc	gtc	agc	gac	att	gat	gcc	gcc	gtt	1104	
Asp	Pro	Ala	Asp	Ile	His	Glu	Ala	Val	Ser	Asp	Ile	Asp	Ala	Ala	Val		
		355					360					365					
gaa	tcg	acc	gag	gca	taaggagaga	cccaagatgg	cta									1142	
Glu	Ser	Thr	Glu	Ala													
		370															

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<212> PRT

<213> Corynebacterium glutamicum

<400> 232

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 His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
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 gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc 144
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45
 ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc 192
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
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 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
 65 70 75 80
 cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt 288
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
 85 90 95
 ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc 336
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
 100 105 110
 gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc 384
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
 115 120 125
 tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa 432
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
 130 135 140
 acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt 480
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
 145 150 155 160
 ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca 528
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
 165 170 175
 cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt 576

290					295					300					
Ile Gly Ile Gly Thr Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr															
305					310					315					320
Ala Phe Gln Asn Pro Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser					325					330					335
Phe Asp Ala Tyr Lys His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala					340					345					350
Arg Glu Ala Ile Val Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val					355					360					365
Ala Glu Asp Tyr Ala Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp					370					375					380
Ala Glu Val Asp Lys Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly					385					390					400
Gln Pro Glu Ile Ile Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp					405					410					415
Val Ile Val Gln Ala Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu					420					425					430
Trp Arg Val Arg Asp Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser					435					440					445
Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu					450					455					460
Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly					465					470					475
Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly					485					490					495
Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile					500					505					510
Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr					515					520					525
Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu					530					535					540
Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile					545					550					555
Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met					565					570					575
Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser					580					585					590
Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro					595					600					605
Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp					610					615					620

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 <213> *Corynebacterium glutamicum*

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 Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly
 35 40 45

 Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr
 50 55 60

 Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr
 65 70 75 80

 Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val
 85 90 95

 Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr
 100 105 110

 Asn Arg Leu Pro Ala Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg
 115 120 125

 Val Ala Asp Pro Val Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly
 130 135 140

 Leu Thr Val Asn Asp Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg
 145 150 155 160

 Val Gln Arg Pro Glu Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg
 165 170 175

 Val Leu Thr Asp Pro Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro
 180 185 190

 Glu Asp Val Gln Ala Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln
 195 200 205

 Asp Arg Glu Trp His Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu
 210 215 220

 Ala Arg Ala Ile Glu Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile
 225 230 235 240

 Ala Gly Gly Gly Val Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala
 245 250 255

 Leu Val Glu Gln Thr Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly
 260 265 270

 Gly Val Leu Ala Trp Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala
 275 280 285

 Thr Gly Thr Leu Ala Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile

265					270					275							
act	atg	atg	aac	acc	ggt	gct	gtg	cac	ggt	gct	gct	ctt	ggc	gca	gct	979	
Thr	Met	Met	Asn	Thr	Gly	Ala	Val	His	Gly	Ala	Ala	Leu	Gly	Ala	Ala		
280					285					290							
gag	gtt	gca	gca	acc	aag	act	gag	ctt	gga	ttc	gat	cct	gag	gct	cac	1027	
Glu	Val	Ala	Ala	Thr	Lys	Thr	Glu	Leu	Gly	Phe	Asp	Pro	Glu	Ala	His		
295					300					305							
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Phe	Ala	Ile	Asp	Asp	Glu	Val	Ile	Ala	His	Thr	Arg	Ser	Leu	Ala	Glu		
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cgc	gct	gca	cag	aag	aag	gct	gca	tgg	cag	gtc	aag	ttc	gat	gag	tgg	1123	
Arg	Ala	Ala	Gln	Lys	Lys	Ala	Ala	Trp	Gln	Val	Lys	Phe	Asp	Glu	Trp		
330					335					340							
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Ala	Ala	Ala	Asn	Pro	Glu	Asn	Lys	Ala	Leu	Phe	Asp	Arg	Leu	Asn	Ser		
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cgt	gag	ctt	cca	gcg	ggc	tac	gct	gac	gag	ctc	cca	aca	tgg	gat	gca	1219	
Arg	Glu	Leu	Pro	Ala	Gly	Tyr	Ala	Asp	Glu	Leu	Pro	Thr	Trp	Asp	Ala		
360					365					370							
gat	gag	aag	ggc	gtc	gca	act	cgt	aag	gct	tcc	gag	gct	gca	ctt	cag	1267	
Asp	Glu	Lys	Gly	Val	Ala	Thr	Arg	Lys	Ala	Ser	Glu	Ala	Ala	Leu	Gln		
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Ala	Leu	Gly	Lys	Thr	Leu	Pro	Glu	Leu	Trp	Gly	Gly	Ser	Ala	Asp	Leu		
390					395					400					405		
gca	ggt	tcc	aac	aac	acc	gtg	atc	aag	ggc	tcc	cct	tcc	ttc	ggc	cct	1363	
Ala	Gly	Ser	Asn	Asn	Thr	Val	Ile	Lys	Gly	Ser	Pro	Ser	Phe	Gly	Pro		
410					415					420							
gag	tcc	atc	tcc	acc	gag	acc	tgg	tct	gct	gag	cct	tac	ggc	cgt	aac	1411	
Glu	Ser	Ile	Ser	Thr	Glu	Thr	Trp	Ser	Ala	Glu	Pro	Tyr	Gly	Arg	Asn		
425					430					435							
ctg	cac	ttc	ggt	atc	cgt	gag	cac	gct	atg	gga	tcc	atc	ctc	aac	ggc	1459	
Leu	His	Phe	Gly	Ile	Arg	Glu	His	Ala	Met	Gly	Ser	Ile	Leu	Asn	Gly		
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Ile	Ser	Leu	His	Gly	Gly	Thr	Arg	Pro	Tyr	Gly	Gly	Thr	Phe	Leu	Ile		
455					460					465							
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Phe	Ser	Asp	Tyr	Met	Arg	Pro	Ala	Val	Arg	Leu	Ala	Ala	Leu	Met	Glu		
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Thr	Asp	Ala	Tyr	Tyr	Val	Trp	Thr	His	Asp	Ser	Ile	Gly	Leu	Gly	Glu		
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Asp	Gly	Pro	Thr	His	Gln	Pro	Val	Glu	Thr	Leu	Ala	Ala	Leu	Arg	Ala		
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Trp	Ser	Asp	Val	Asp	Thr	Lys	Ala	Val	Asp	Thr	Val	Arg	Val	Leu	Ala		
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Ala	Asp	Ala	Val	Glu	Asn	Cys	Gly	Ser	Gly	His	Pro	Gly	Thr	Ala	Met		
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Asp	Pro	Gln	Asp	Thr	Asn	Trp	Ala	Gly	Arg	Asp	Arg	Phe	Val	Leu	Ser		
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Cys	Gly	His	Ser	Ser	Leu	Thr	Gln	Tyr	Ile	Gln	Leu	Tyr	Leu	Gly	Gly		
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Phe	Gly	Leu	Glu	Met	Asp	Asp	Leu	Lys	Ala	Leu	Arg	Thr	Trp	Asp	Ser		
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Leu	Thr	Pro	Gly	His	Pro	Glu	Tyr	Arg	His	Thr	Lys	Gly	Val	Glu	Ile		
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acc	act	ggc	cct	ctt	ggc	cag	ggt	ctt	gca	tct	gca	gtt	ggt	atg	gcc	547	
Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Leu	Ala	Ser	Ala	Val	Gly	Met	Ala		
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Gly	Glu	Ser	Pro	Phe	Asp	His	His	Ile	Tyr	Val	Ile	Ala	Ser	Asp	Gly		
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gac	ctg	cag	gaa	ggt	gtc	acc	tct	gag	gca	tcc	tcc	atc	gct	ggc	acc	691	
Asp	Leu	Gln	Glu	Gly	Val	Thr	Ser	Glu	Ala	Ser	Ser	Ile	Ala	Gly	Thr		
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Gln	Gln	Leu	Gly	Asn	Leu	Ile	Val	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser		
			200				205					210					
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Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg		
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tac	aag	gct	tac	ggc	tgg	cag	acc	att	gag	gtt	gag	gct	ggc	gag	gac	835	
Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp		
					235				240					245			
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Val	Ala	Ala	Ile	Glu	Ala	Ala	Val	Ala	Glu	Ala	Lys	Lys	Asp	Thr	Lys		
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cga	cct	acc	ttc	atc	cgc	gtt	cgc	acc	atc	atc	ggc	ttc	cca	gct	cca	931	
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Leu Thr Thr Leu Thr
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ctg tca cct gaa ctt cag gcg ctc act gta cgc aat tac ccc tct gat 163
Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg Asn Tyr Pro Ser Asp
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tgg tcc gat gtg gac acc aag gct gta gac act gtt cgt gtc ctc gct 211

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Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr
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aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075
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ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val
 330 335 340

gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171
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 Arg Leu Lys
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 35 40 45

Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
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Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
 65 70 75 80

Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
 85 90 95

Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
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Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
 115 120 125

Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
 130 135 140

Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
 145 150 155 160

Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala

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Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Met Ser	
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Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly	
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Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg	
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Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr	
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Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg	
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Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg	
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Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala	
135 140 145	
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Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile	
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Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly	
170 175 180	
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Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser	
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Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg	
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Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg Gly Lys Ala	
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Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp	
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Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val	
265 270 275	
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 370 375 380
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 385 390 395 400
 Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser
 405 410 415
 Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
 420 425 430
 Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg
 435 440 445
 Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
 450 455 460
 Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala
 465 470 475 480
 Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly
 485 490 495
 Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg
 500 505 510
 Arg Pro

<210> 245
 <211> 1203
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1180)
 <223> RXA02738

<400> 245
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 cacagttcaa gaacaattct tttaaggaaa atttagtttc atg tct cac att gat 115
 Met Ser His Ile Asp
 1 5
 gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac ctc tcc cgc 163
 Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg
 10 15 20
 gag cgc att act tcc ggc aat ctc agc cag gtt att gag gaa aag tct 211
 Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser
 25 30 35

Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val
 20 25 30

Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala
 35 40 45

Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
 50 55 60

Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
 65 70 75 80

Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
 85 90 95

Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
 100 105 110

Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
 115 120 125

Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
 130 135 140

Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
 145 150 155 160

Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys
 165 170 175

Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val
 180 185 190

Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu
 195 200 205

Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
 210 215 220

Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile
 225 230 235 240

Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
 245 250 255

Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu
 260 265 270

Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln
 275 280 285

Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr
 290 295 300

Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
 305 310 315 320

Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro
 325 330 335

Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser

aag gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag 1123
Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu
330 335 340

act ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt 1171
Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly
345 350 355

gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act 1219
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr
360 365 370

gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc 1267
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly
375 380 385

gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag 1315
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln
390 395 400 405

cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct 1363
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser
410 415 420

gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc 1411
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser
425 430 435

ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg 1459
Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala
440 445 450

ctg tta gat gaa tcc agc ctc ttc cct acc aac gag gaa gtg gaa ctg 1507
Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu
455 460 465

agc tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga 1555
Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly
470 475 480 485

gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat 1603
Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp
490 495 500

gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg 1652
Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro
505 510

gcaaaaaatg atc 1665

<210> 244

<211> 514

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Val Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp
1 5 10 15

70	75	80	85	
agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc				403
Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu	90	95	100	
gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct				451
Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Asp Ala Ala	105	110	115	
ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc				499
Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly	120	125	130	
acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc				547
Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile Pro Pro Asp Ser Phe	135	140	145	
aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc				595
Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr	150	155	160	165
gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac				643
Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn	170	175	180	
ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca				691
Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro	185	190	195	
gaa tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt				739
Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val	200	205	210	
caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg				787
Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu	215	220	225	
tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat				835
Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp	230	235	240	245
att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc				883
Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala	250	255	260	
cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc				931
Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala	265	270	275	
atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag				979
Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys	280	285	290	
atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc				1027
Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr	295	300	305	
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc				1075
Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val	310	315	320	325

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
 225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
 245 250 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
 260 265 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

<210> 243
 <211> 1665
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1642)
 <223> RXA02737

<400> 243
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acacatcttt cattaaagaa aggatcgtga cactaccatc gtg agc aca aac acg 115
 Val Ser Thr Asn Thr
 1 5

acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga 163
 Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg
 10 15 20

ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act 211
 Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr
 25 30 35

ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259
 Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala
 40 45 50

aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc 307
 Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg
 55 60 65

cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355
 Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala

Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile
 295 300 305

gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
 310 315 320 325

gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
 330 335

taatgccaac agcaagccca att 1140

<210> 242

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
 1 5 10 15

Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
 20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
 35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
 50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
 65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
 85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
 100 105 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
 115 120 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
 130 135 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
 145 150 155 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
 165 170 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
 180 185 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
 195 200 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
 210 215 220

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc	307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile	
55 60 65	
gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt	355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val	
70 75 80 85	
gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt	403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg	
90 95 100	
gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct	451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser	
105 110 115	
tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt	499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu	
120 125 130	
gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc	547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly	
135 140 145	
tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat	595
Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp	
150 155 160 165	
ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta	643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu	
170 175 180	
gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc	691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala	
185 190 195	
cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac	739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His	
200 205 210	
tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt	787
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu	
215 220 225	
ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt	835
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu	
230 235 240 245	
tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc	883
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile	
250 255 260	
gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg	931
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met	
265 270 275	
aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg	979
Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr	
280 285 290	
gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att	1027

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
 100 105 110
 His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
 115 120 125
 Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
 130 135 140
 Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
 145 150 155 160
 Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
 165 170 175
 Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
 180 185 190
 Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
 195 200 205
 His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
 210 215 220
 Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
 225 230 235 240
 Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
 245 250

<210> 241

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1117)

<223> RXS01758

<400> 241

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 gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
 Met Pro Lys Tyr Ile 5
 1

 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val 20
 10 15

 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala 35
 25 30

 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys 50
 40 45

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499
 Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
 120 125 130

tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547
 Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
 135 140 145

gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595
 Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
 150 155 160 165

cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643
 Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
 170 175 180

ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691
 Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
 185 190 195

gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg 739
 Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
 200 205 210

tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787
 Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
 215 220 225

ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt 835
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
 230 235 240 245

gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876
 Ala Arg Leu Ile Ala Gly
 250

<210> 240

<211> 251

<212> PRT

<213> Corynebacterium glutamicum.

<400> 240

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
 1 5 10 15

Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
 20 25 30

Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
 35 40 45

Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
 50 55 60

Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65 70 75 80

Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
 85 90 95

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser
 465 470 475 480

Glu Val Glu Ala

<210> 253
 <211> 1537
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1537)
 <223> FRXA00999

<400> 253
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ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
 Met Thr Asn Gly Asp
 1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc 499
 Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser
 120 125 130

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125
 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140
 Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430

tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc 1219
 Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys
 360 365 370
 atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385
 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405
 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420
 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435
 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450
 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465
 tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct 1552
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser Glu Val Glu Ala
 470 475 480
 taaaggctct ccttttaaca caa 1575

<210> 252

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
 1 5 10 15
 Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30
 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45
 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60
 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80
 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95
 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc	499
Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser	
120 125 130	
ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc	547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
135 140 145	
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
150 155 160 165	
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc	643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
170 175 180	
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac	691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc	787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
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Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	

Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro
 180 185 190

Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val
 195 200 205

Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser
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Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp
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Leu

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 <223> RXN00999

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 Met Thr Asn Gly Asp
 1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
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ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser
 165 170 175

 caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr
 180 185 190 195

 cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser
 200 205 210

 ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val
 215 220 225

 act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770
 Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu
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 tagtttccac acattcttaa atg 793

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 250

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 20 25 30

 Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His
 35 40 45

 Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met
 50 55 60

 His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu
 65 70 75 80

 Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala
 85 90 95

 Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp
 100 105 110

 Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln
 115 120 125

 Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu
 130 135 140

 Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp
 145 150 155 160

 Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys
 165 170 175

675

680

685

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690 695 700

<210> 249

<211> 793

<212> DNA

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<220>

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<222> (48) .. (770)

<223> RXA00965

<400> 249

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Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly
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aca tcc cac tac tcc cgt cag ctc tcc ctc gtg gac aac gct gag ttc 152
Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe
20 25 30 35

ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc 200
Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala
40 45 50

cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca 248
His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala
55 60 65

aat act ggt gag gaa acc cca atg tac gtg tgc cca gaa gcg cgc aac 296
Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn
70 75 80

gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac 344
Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn
85 90 95

ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg 392
Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr
100 105 110 115

tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act 440
Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr
120 125 130

gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc 488
Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile
135 140 145

cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag 536
His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu
150 155 160

Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu
 355 360 365
 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser
 370 375 380
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly
 385 390 395 400
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser
 405 410 415
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu
 420 425 430
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly
 435 440 445
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly
 450 455 460
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu
 465 470 475 480
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser
 485 490 495
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu
 500 505 510
 Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp
 515 520 525
 Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu
 530 535 540
 Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu
 545 550 555 560
 Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val
 565 570 575
 Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser
 580 585 590
 Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala
 595 600 605
 Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe
 610 615 620
 Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val
 625 630 635 640
 Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg
 645 650 655
 Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala
 660 665 670
 Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His
 35 40 45
 Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln
 50 55 60
 Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp
 65 70 75 80
 Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln
 85 90 95
 Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu
 100 105 110
 Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr
 115 120 125
 Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser
 130 135 140
 Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp
 145 150 155 160
 Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val
 165 170 175
 Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser
 180 185 190
 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp
 195 200 205
 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu
 210 215 220
 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val
 225 230 235 240
 Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala
 245 250 255
 Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile
 260 265 270
 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala
 275 280 285
 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe
 290 295 300
 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr
 305 310 315 320
 Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val
 325 330 335
 Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe
 340 345 350

atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc 1699
 Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala
 520 525 530

cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt 1747
 Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu
 535 540 545

gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag 1795
 Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys
 550 555 560 565

gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc 1843
 Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser
 570 575 580

aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag 1891
 Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln
 585 590 595

ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct 1939
 Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala
 600 605 610

cgc gtt gtt tcc gtt cct tgc atg gat tgg ttc cag gag cag gac gca 1987
 Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala
 615 620 625

gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct 2035
 Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser
 630 635 640 645

gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag 2083
 Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln
 650 655 660

ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag 2131
 Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln
 665 670 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg 2179
 Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala
 680 685 690

gcc aag gac tcc att aac ggt taattgccct gctgttttta gct 2223
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<211> 700

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<213> Corynebacterium glutamicum

<400> 248

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Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr
 20 25 30

Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
 280 285 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc 1027
 Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
 295 300 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc 1075
 Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
 310 315 320 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa 1123
 Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
 330 335 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa 1171
 Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
 345 350 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg 1221
 Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 360 365

gca 1224

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 <211> 367
 <212> PRT
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<400> 264
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 20 25 30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
 35 40 45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
 50 55 60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65 70 75 80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
 85 90 95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
 100 105 110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
 115 120 125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
 130 135 140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
 145 150 155 160

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg	259
Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu	
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ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat	307
Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn	
55 60 65	
ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa	355
Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu	
70 75 80 85	
acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat	403
Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp	
90 95 100	
gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc	451
Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly	
105 110 115	
ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc	499
Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala	
120 125 130	
acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta	547
Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val	
135 140 145	
ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg	595
Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp	
150 155 160 165	
gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa	643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys	
170 175 180	
ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc	691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr	
185 190 195	
gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta	739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu	
200 205 210	
gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc	787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val	
215 220 225	
cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa	835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu	
230 235 240 245	
cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca	883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro	
250 255 260	
atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa	931
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu	
265 270 275	
ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc	979

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tacgcgttgc catgaggata agactaccgt tagtgggggtg   ttg gat tca tcg cta    115
                                     Leu Asp Ser Ser Leu
                                      1                      5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctg gat tcg gaa gtc    163
Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu Leu Asp Ser Glu Val
                        10                          15                  20

act ttc gcc gat ctg acg acc ctc cgc atc ggc gga aaa ccc cgc agc    211
Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly Gly Lys Pro Arg Ser
                        25                          30                  35
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Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
 35 40 45
 ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc 192
 Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
 50 55 60
 ttg cgt gag gtc gat tcc atc aat atg cgt cgt cgc gac cgt gtg gtg 240
 Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val
 65 70 75 80
 cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg gcc aag cgg gtt 288
 Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
 85 90 95
 aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat 336
 Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
 100 105 110
 tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg 384
 Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
 115 120 125
 gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc 432
 Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
 130 135 140
 ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc 480
 Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
 145 150 155 160
 cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac 528
 His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
 165 170 175
 ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat gcc 576
 Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
 180 185 190
 cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg 624
 Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
 195 200 205
 gaa gcg ctc ggc cgc aac ctt tagtgcggtg gatcaggcgg ggc 668
 Glu Ala Leu Gly Arg Asn Leu
 210 215

<210> 262

<211> 215

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

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Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala

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<400> 260
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 20 25 30
 Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45
 Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60
 Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80
 Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95
 Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110
 Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125
 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140
 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160
 Thr Ala Lys Gln Trp Gln
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<210> 261
 <211> 668
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(645)
 <223> RXA02572

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 Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu
 1 5 10 15
 gtg gat gcc atc ggt cac gac gat cgt atc ggc cga aag ttc tta ggc 96
 Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
 20 25 30
 gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct 144

gac gac cga gac atg ctg aag cag tac cgc ctt ctg gct gct gaa gag 336
 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 gct gct aat aat aag gtg ctg ttc ggc ggt cga ctg ggc acg tac cag 384
 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 tac ctc gac atg cac atg gct atc ggt tct gcg ctg agc atg ttt gac 432
 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 aac aag ctg gtg ccg ttc ttt gaa gaa ggc aca ccg cta gag cag gaa 480
 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

 cgc gga cac taaaaggaag ggcatctccc aca 512
 Arg Gly His

<210> 258
 <211> 163
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 258
 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
 1 5 10 15

 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30

 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45

 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60

 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80

 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

 Arg Gly His

Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp
 290 295 300
 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe
 305 310 315 320
 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp
 325 330 335
 Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala
 340 345 350
 Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu
 355 360 365
 Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys
 370 375 380
 Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly
 385 390 395 400
 His

<210> 257
 <211> 512
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(489)
 <223> FRXA02596

<400> 257
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 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
 1 5 10 15
 ggc aag ctg gga tgg cgc acc ctc gac ttt gaa acc gaa gta gta gaa 96
 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30
 acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac 144
 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45
 gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt 192
 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60
 gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc 240
 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80
 cgt ttc gca gat aac gag gat gag cct tat tac cca atc aac act cca 288
 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

<210> 256

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu
 1 5 10 15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
 20 25 30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn
 165 170 175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn
 180 185 190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu
 195 200 205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp
 210 215 220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val
 225 230 235 240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys
 245 250 255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly
 260 265 270

Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro
 275 280 285

cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca	643
Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro	
170 175 180	
gtt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc	691
Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly	
185 190 195	
ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat	739
Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu Lys Met Ala Glu His	
200 205 210	
gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat	787
Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp	
215 220 225	
gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca	835
Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro	
230 235 240 245	
ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc	883
Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr	
250 255 260	
ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc	931
Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr	
265 270 275	
cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac	979
Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His	
280 285 290	
gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat	1027
Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp	
295 300 305	
aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat	1075
Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp	
310 315 320 325	
gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag	1123
Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys	
330 335 340	
cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg	1171
Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu	
345 350 355	
ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct	1219
Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala	
360 365 370	
atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt	1267
Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe	
375 380 385	
gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag	1313
Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His	
390 395 400	
ggcatctccc aca	1326

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 465 470 475

<210> 255
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02596

<400> 255
 aaggtatctg ggtgtggata tgccctgcta actggagaaa cttggcccga tcgggtgtct 60

gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115
 Met Thr Glu Ser Lys
 1 5

aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
 10 15 20

gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
 25 30 35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
 Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
 40 45 50

acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
 55 60 65

aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
 70 75 80 85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
 90 95 100

ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
 105 110 115

cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
 120 125 130

tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
 135 140 145

cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
 150 155 160 165

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

 tcc ttc cac acc gag tgg tcc ggc gac cgc 1537
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 470 475

<210> 254

<211> 479

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
 1 5 10 15

 Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30

 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

 Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125

 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140

ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly 135 140 145	547
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala 150 155 160 165	595
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly 170 175 180	643
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp 185 190 195	691
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly 200 205 210	739
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly 215 220 225	787
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln 230 235 240 245	835
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala 250 255 260	883
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp 265 270 275	931
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala 280 285 290	979
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro 295 300 305	1027
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln 310 315 320 325	1075
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala 330 335 340	1123
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn 345 350 355	1171
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys 360 365 370	1219

Leu Glu Ile Glu Tyr Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly
 85 90 95
 Gly Ile Arg Asn Val Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val
 100 105 110
 Phe Asn Gly Asp Val Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp
 115 120 125
 Thr His Arg Glu Lys Asp Ala Asp Leu Thr Met His Leu Val Arg Val
 130 135 140
 Ala Asn Pro Arg Ala Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg
 145 150 155 160
 Val Ser Glu Phe Leu Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile
 165 170 175
 Asn Ala Gly Cys Tyr Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro
 180 185 190
 Ala Gly Arg Ala Val Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu
 195 200 205
 Glu Glu Gly Lys Arg Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg
 210 215 220
 Asp Met Gly Thr Pro Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val
 225 230 235 240
 Arg Gly Ile Ala Tyr Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser
 245 250 255
 Leu Val Asp Ala Ser Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly
 260 265 270
 Gly Thr Val Val Gly Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val
 275 280 285
 Asp Asn Thr Val Ile Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val
 290 295 300
 Ile Glu Asn Ser Ile Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala
 305 310 315 320
 His Ile Ser Gly Cys Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg
 325 330 335
 Cys Glu Leu Asn Ala Gly Met Arg Val Phe Pro Gly Val Val Ile Pro
 340 345 350
 Asp Ser Gly Ile Arg Phe Ser Ser Asp Gln
 355 360

<210> 275

<211> 1350

<212> DNA

<213> Corynebacterium glutamicum

<220>

Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro
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 agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac 835
 Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr
 230 235 240 245
 tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc 883
 Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser
 250 255 260
 gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc 931
 Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly
 265 270 275
 cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att 979
 Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile
 280 285 290
 ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc 1027
 Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile
 295 300 305
 att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc 1075
 Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys
 310 315 320 325
 atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca 1123
 Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg Cys Glu Leu Asn Ala
 330 335 340
 ggg atg cgc gtc ttc cca ggc gtt gtg atc cca gac agc gga att cgt 1171
 Gly Met Arg Val Phe Pro Gly Val Ile Pro Asp Ser Gly Ile Arg
 345 350 355
 ttt tcg tct gat cag taggcatttt tagccctttt gga 1209
 Phe Ser Ser Asp Gln
 360
 <210> 274
 <211> 362
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 274
 Met Thr Leu Thr Asp Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val
 1 5 10 15
 Gly Gly Lys Gly Thr Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys
 20 25 30
 Pro Met Leu Pro Thr Ala Gly His Pro Phe Leu Thr His Leu Leu Ala
 35 40 45
 Arg Ile Lys Ala Ala Gly Ile Thr His Val Val Leu Gly Thr Ser Phe
 50 55 60
 Lys Ala Glu Val Phe Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly
 65 70 75 80

tgaaatggat ttgctgcggc cccggaatta cccttttcgc ggccgtcatc aaatttgtac 60

gtc ttc ggc cac gtc gac gct tcc tac tgg cgc qac atg ggc acc cca 787

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg
 130 135 140
 Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val
 145 150 155 160
 Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu
 165 170 175
 Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala
 180 185 190
 Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala
 195 200 205
 Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr
 210 215 220
 Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His
 225 230 235 240
 Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp
 245 250 255
 Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile
 260 265 270
 Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu
 275 280 285
 Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val
 290 295 300
 Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val
 305 310 315 320
 Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro
 325 330 335
 Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile
 340 345 350
 Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr
 355 360 365
 Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe
 370 375 380
 Gln Arg Asp
 385

<210> 273
 <211> 1209
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1186)
 <223> RXA01377

gca aat aag act cgt aag gac ttt att gca gag gat atc ctc agt aaa 979
 Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu Asp Ile Leu Ser Lys
 280 285 290

tca cct act gta gtt gga att tac cgc ctt gta atg aag tct gga tca 1027
 Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val Met Lys Ser Gly Ser
 295 300 305

gat aac ttt cgt tct tct tct att caa gga gtc atg aaa cga att aag 1075
 Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val Met Lys Arg Ile Lys
 310 315 320 325

gcc aag gga atc gaa att gta gta ttt gaa ccg aat ctc gga gaa gaa 1123
 Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro Asn Leu Gly Glu Glu
 330 335 340

act ttc tac aat tcg aag atc ctt aat gac atc gaa gag ttt aag gat 1171
 Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile Glu Glu Phe Lys Asp
 345 350 355

tac tgc gac atc att att gca aat cgt cca acc gat gag ctt tct gat 1219
 Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr Asp Glu Leu Ser Asp
 360 365 370

gta cca gaa aaa gtt tat aca cgt gat att ttc cag cgt gac 1261
 Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe Gln Arg Asp
 375 380 385

taagtggaaa gaatcttttg ttg 1284

<210> 272

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Ile Ala Val Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala
 1 5 10 15

Ala Leu Leu Ser Lys Asn His Lys Val Val Ala Val Asp Ile Asp Glu
 20 25 30

Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser
 35 40 45

Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr
 50 55 60

Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala
 65 70 75 80

Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser
 85 90 95

Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr
 100 105 110

Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg
 115 120 125

gtt caa gaa ttt cgt tgc cca att gtc gat agc gat ctc gaa gaa tat	259
Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser Asp Leu Glu Glu Tyr	
40 45 50	
ctg tcc act aag cct caa aac tta act gcc aca acg gac gcc gaa gcc	307
Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr Thr Asp Ala Glu Ala	
55 60 65	
gct tac aaa ggc gca gat ttt att gtt att gca acg cca act aat tac	355
Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala Thr Pro Thr Asn Tyr	
70 75 80 85	
gac cca gag tca aac ttt ttt gat act tcc agc gtt gag tcc gta att	403
Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser Val Glu Ser Val Ile	
90 95 100	
gag ata gtc ctt aag gtt tct cct gga tcc aca atc gta att aaa tcg	451
Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr Ile Val Ile Lys Ser	
105 110 115	
act atc cct gtt ggt ttt aca tcg gaa cta cgc att aag cat cca gaa	499
Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg Ile Lys His Pro Glu	
120 125 130	
gct tcg att att ttt tca cct gag ttc ctg cgt gaa ggc cga gca ttc	547
Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Arg Ala Phe	
135 140 145	
tac gac aat ctc tac cca tcc aga gtt gtc gtt ggt gat cgc agt cct	595
Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val Gly Asp Arg Ser Pro	
150 155 160 165	
ctg ggg gaa gaa ttt gcg act ctg tta gct gag ggg gca aaa gaa aag	643
Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu Gly Ala Lys Glu Lys	
170 175 180	
cct ccg att cta ctt acg gac tca act gag gca gag gcg att aaa tta	691
Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala Glu Ala Ile Lys Leu	
185 190 195	
ttt tct aat aca tat ctt gca ctg cga gtt gct ttt ttc aac gaa ctg	739
Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala Phe Phe Asn Glu Leu	
200 205 210	
gat act tat gcg tct gtt cga agc ttg gat act aag cag att att gaa	787
Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr Lys Gln Ile Ile Glu	
215 220 225	
ggg gta ggg ctc gat cca cgt att gga tct cat tac aat aat cct tca	835
Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His Tyr Asn Asn Pro Ser	
230 235 240 245	
ttt gga tat ggc gga tat tgt ctt ccg aaa gat acg aaa cag ctt ctc	883
Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp Thr Lys Gln Leu Leu	
250 255 260	
gcc aac tat aag gat gtc ccg cag aat cta atc tct gca gta gtc caa	931
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<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

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 20 25 30

Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu
 35 40 45

Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile
 50 55 60

Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser
 65 70 75 80

Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu
 85 90 95

Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln
 100 105 110

Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val
 115 120 125

Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His
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<210> 271

<211> 1284

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1261)

<223> RXA01262

<400> 271

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 Met Lys Ile Ala Val
 1 5

gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163
 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys
 10 15 20

aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta 211
 Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu
 25 30 35

Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile
 245 250 255

Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys
 260 265 270

Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser
 275 280 285

<210> 269
 <211> 526
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(526)
 <223> RXA02028

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 Met Ser Leu Pro Ile
 1 5

gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga 163
 Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly
 10 15 20

ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg 211
 Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu
 25 30 35

ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct 259
 Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala
 40 45 50

gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa 307
 Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 55 60 65

gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg 355
 Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr
 70 75 80 85

ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc 403
 Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala
 90 95 100

gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg 451
 Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly
 105 110 115

cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa 499
 Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 120 125 130

gat gtc gta gcg gtg atg ttg ccg cac 526
 Asp Val Val Ala Val Met Leu Pro His

Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val
 265 270 275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc 978
 Lys Glu Ile Leu Ala Glu Phe Glu Ser
 280 285

aca 981

<210> 268

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu
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Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala
 20 25 30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 35 40 45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr
 50 55 60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala
 65 70 75 80

Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly
 85 90 95

Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 100 105 110

Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly
 115 120 125

Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val
 130 135 140

Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val
 145 150 155 160

Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg
 165 170 175

Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser
 180 185 190

Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp
 195 200 205

Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr
 210 215 220

Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val
 225 230 235 240

acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca	211
Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala	
25 30 35	
act cgg tta gca att atc act gct ccg aac aaa gac gga att ctt aaa	259
Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys	
40 45 50	
cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt	307
His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly	
55 60 65	
aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca	355
Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Arg Glu Leu Ile Ala	
70 75 80 85	
aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt	403
Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val	
90 95 100	
ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc	451
Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val	
105 110 115	
atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg	499
Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met	
120 125 130	
gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag	547
Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu	
135 140 145	
gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa	595
Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu	
150 155 160 165	
ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg	643
Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met	
170 175 180	
gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg	691
Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr	
185 190 195	
ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att	739
Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile	
200 205 210	
gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta	787
Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu	
215 220 225	
ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag	835
Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys	
230 235 240 245	
cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac	883
Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile Pro Ala Val Val Tyr	
250 255 260	
ttc gga ctt cgt cat gca gag tac ggt tcc aag att cac cgt gcg gtg	931

Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
 165 170 175

Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
 180 185 190

Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
 195 200 205

Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
 210 215 220

Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
 225 230 235 240

Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
 245 250 255

Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
 260 265 270

Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
 275 280 285

Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
 290 295 300

Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile
 305 310 315 320

Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln
 325 330 335

Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala
 340 345 350

Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly
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<210> 267

<211> 981

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(958)

<223> RXA01259

<400> 267

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tcaaaatgct gtaaaaactg tcgtggtacc agctgcagga atg gga aca cgg ttc 115
 Met Gly Thr Arg Phe
 1 5

ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat 163
 Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp
 10 15 20

275	280	285	
acc atc ggc agc cac gtt cgc act ggt tct gac		acc atg ttt atc gct	912
Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp		Thr Met Phe Ile Ala	
290	295	300	
cca gtg acc gtg ggt gac gga gcg tat tcc gga gcc ggt aca gta att			960
Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile			
305	310	315	320
aaa gac gat gtt ccg cca gga gcc ctt gcc gtg tcc ggc gga cgc caa			1008
Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln			
	325	330	335
cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca			1056
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala			
	340	345	350
gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc			1101
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly			
	355	360	365
taagcaggat cctcatgact gct			1124
<210> 266			
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Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr			
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Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu			
	35	40	45
Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser			
	50	55	60
Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu			
	65	70	75
Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu			
	85	90	95
Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala			
	100	105	110
Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu			
	115	120	125
Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly			
	130	135	140
Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val			
	145	150	155
			160

Gly	Arg	Ile	Val	Arg	Asn	Glu	Glu	Gly	Glu	Val	Thr	Ala	Ile	Val	Glu		
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caa	aaa	gat	gct	tca	gca	gaa	gtc	caa	gcc	atc	gat	gag	gtc	aac	tcc	192	
Gln	Lys	Asp	Ala	Ser	Ala	Glu	Val	Gln	Ala	Ile	Asp	Glu	Val	Asn	Ser		
	50					55				60							
ggt	gtc	ttt	gct	ttc	gac	gcc	gcc	atc	ttg	cgt	tcc	gca	ctg	gct	gaa	240	
Gly	Val	Phe	Ala	Phe	Asp	Ala	Ala	Ile	Leu	Arg	Ser	Ala	Leu	Ala	Glu		
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Leu	Lys	Ser	Asp	Asn	Ala	Gln	Gly	Glu	Leu	Tyr	Leu	Thr	Asp	Val	Leu		
				85				90						95			
ggc	att	gct	cgt	ggc	gag	ggc	cac	cca	gtg	cgc	gcc	cac	acc	gcc	gcc	336	
Gly	Ile	Ala	Arg	Gly	Glu	Gly	His	Pro	Val	Arg	Ala	His	Thr	Ala	Ala		
		100						105					110				
gat	gct	cgt	gaa	ctc	gcc	ggc	gtc	aac	gat	cgt	gtg	cag	ctc	gca	gaa	384	
Asp	Ala	Arg	Glu	Leu	Ala	Gly	Val	Asn	Asp	Arg	Val	Gln	Leu	Ala	Glu		
		115					120					125					
gcc	ggc	gcc	gaa	cta	aac	cgt	cgc	acc	gtc	atc	gcc	gct	atg	cgt	ggt	432	
Ala	Gly	Ala	Glu	Leu	Asn	Arg	Arg	Thr	Val	Ile	Ala	Ala	Met	Arg	Gly		
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Gly	Ala	Thr	Ile	Val	Asp	Pro	Ala	Thr	Thr	Trp	Ile	Asp	Val	Glu	Val		
145					150					155				160			
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Ser	Ile	Gly	Arg	Asp	Val	Ile	Ile	His	Pro	Gly	Thr	Gln	Leu	Lys	Gly		
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gaa	act	gtc	atc	gga	gac	cgc	gtt	gaa	gtt	ggt	cca	gac	acc	acc	ttg	576	
Glu	Thr	Val	Ile	Gly	Asp	Arg	Val	Glu	Val	Gly	Pro	Asp	Thr	Thr	Leu		
			180					185					190				
acc	aac	atg	acc	atc	ggc	gac	ggc	gca	tcc	gta	atc	cgc	acc	cac	ggt	624	
Thr	Asn	Met	Thr	Ile	Gly	Asp	Gly	Ala	Ser	Val	Ile	Arg	Thr	His	Gly		
		195					200					205					
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Phe	Asp	Ser	Thr	Ile	Gly	Glu	Asn	Ala	Thr	Val	Gly	Pro	Phe	Thr	Tyr		
	210					215					220						
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Ile	Arg	Pro	Gly	Thr	Thr	Leu	Gly	Pro	Glu	Gly	Lys	Leu	Gly	Gly	Phe		
225					230					235				240			
gta	gaa	acc	aag	aag	gcc	aca	atc	ggc	cgt	ggc	tcc	aag	gtt	cca	cac	768	
Val	Glu	Thr	Lys	Lys	Ala	Thr	Ile	Gly	Arg	Gly	Ser	Lys	Val	Pro	His		
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ctc	acc	tat	gtc	ggc	gac	gcc	acc	atc	ggc	gag	gaa	tcc	aac	atc	gga	816	
Leu	Thr	Tyr	Val	Gly	Asp	Ala	Thr	Ile	Gly	Glu	Glu	Ser	Asn	Ile	Gly		
			260					265					270				
gcc	tcc	tct	gtc	ttc	gtg	aac	tac	gac	ggt	gaa	aac	aag	cac	cac	acc	864	
Ala	Ser	Ser	Val	Phe	Val	Asn	Tyr	Asp	Gly	Glu	Asn	Lys	His	His	Thr		

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
 165 170 175
 Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
 180 185 190
 Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
 195 200 205
 Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
 210 215 220
 Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
 225 230 235 240
 Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
 245 250 255
 Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
 260 265 270
 Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
 275 280 285
 Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
 290 295 300
 Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
 305 310 315 320
 Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
 325 330 335
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 <211> 1124
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(1101)
 <223> RXA01216

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 acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96
 Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
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 ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag 144

tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc 739
 Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg
 200 205 210

ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg 787
 Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met
 215 220 225

tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac 835
 Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn
 230 235 240 245

atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca 883
 Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr
 250 255 260

gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac 931
 Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr
 265 270 275

gga aac tac ctg ctg aga gct ttg taatttacgg tgtggttggtg gag 978
 Gly Asn Tyr Leu Leu Arg Ala Leu
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<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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 35 40 45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
 50 55 60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65 70 75 80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
 85 90 95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
 100 105 110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
 115 120 125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val
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Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro
 145 150 155 160

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(955)

<223> RXA01570

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                                   Val Lys Gly Ile Ile
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Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
                                   10                               20

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Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
                                   25                               35

ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259
Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
                                   40                               50

acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307
Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser
                                   55                               65

tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga 355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly
  70                               75                               80                               85

cta gcc caa gca ttc atc atc ggc gag gaa ttc atc ggt gac gac gac 403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp
                                   90                               95                               100

gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc 451
Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly
                                   105                               110                               115

cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct 499
His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala
                                   120                               125                               130

tat gag gtc tcc gat cct gag cgt tat ggc gtg gtg gaa ttt gat gct 547
Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala
                                   135                               140                               145

gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc 595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser
  150                               155                               160                               165

aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac 643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
                                   170                               175                               180

atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc 691
Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr
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<210> 280
 <211> 260
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 280

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Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu
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Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
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Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
      35           40           45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
 50           55           60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
 65           70           75           80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
          85           90           95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
      100           105           110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
      115           120           125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
      130           135           140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
      145           150           155           160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
          165           170           175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
      180           185           190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
      195           200           205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
      210           215           220

Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His
      225           230           235           240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu
          245           250           255

Asp Arg Leu Lys
          260
  
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<210> 281
 <211> 978
 <212> DNA

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Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu			
40	45	50	
cgc gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa			307
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu			
55	60	65	
gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac			355
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp			
70	75	80	85
ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca			403
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala			
90	95	100	
acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc			451
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile			
105	110	115	
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc			499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly			
120	125	130	
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc			547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser			
135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
170	175	180	
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
185	190	195	
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
200	205	210	
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
215	220	225	
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
230	235	240	245
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
250	255	260	
tagactcccg gggttttgctt ggt			903

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<400> 279
catcaaagtg accgccggcg gcgtcgaatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaactttaa gcgcactaga ctagcaacac atg agc aaa tat gca 115
                                         Met Ser Lys Tyr Ala
                                         1                               5

gac gat tta gcc tta gcc ctc gaa ctc gcc gaa ctt gcc gat tcc atc 163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
                        10                        15                        20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro

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105	110	115	
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc			499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly			
120	125	130	
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc			547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser			
135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
170	175	180	
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
185	190	195	
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
200	205	210	
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
215	220	225	
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
230	235	240	245
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
250	255	260	
tagactcccg ggttttgctt ggt			903

<210> 278

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

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Leu	Ala	Asp	Ser	Ile	Thr	Leu	Asp	Arg	Phe	Glu	Ala	Ser	Asp	Leu	Glu
	20						25						30		
Val	Ser	Ser	Lys	Pro	Asp	Met	Thr	Pro	Val	Ser	Asp	Ala	Asp	Leu	Ala
	35						40					45			
Thr	Glu	Glu	Ala	Leu	Arg	Glu	Lys	Ile	Ala	Thr	Ala	Arg	Pro	Ala	Asp
	50					55				60					
Ser	Ile	Leu	Gly	Glu	Glu	Phe	Gly	Gly	Asp	Val	Glu	Phe	Ser	Gly	Arg
65				70					75					80	

	325		330		335
Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val	340		345		350
Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala	355		360		365
Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val	370		375		380
Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val	385		390		395
Val Val Val Gly Lys Asn Gln Val Val	405				

<210> 277

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN00014

<400> 277

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tgagatctcc gaaacttta ggcactaga ctaacaacac atg agc aaa tat gca	115
Met Ser Lys Tyr Ala	
1 5	

gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc	163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile	
10 15 20	

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca	211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro	
25 30 35	

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc	259
Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu	
40 45 50	

cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa	307
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu	
55 60 65	

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac	355
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp	
70 75 80 85	

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca	403
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala	
90 95 100	

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc	451
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile	

Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu
 1 5 10 15
 Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala
 20 25 30
 Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
 35 40 45
 Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr
 50 55 60
 Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
 65 70 75 80
 Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
 85 90 95
 Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
 100 105 110
 Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
 115 120 125
 Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
 130 135 140
 His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
 145 150 155 160
 Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
 165 170 175
 Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
 180 185 190
 Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
 195 200 205
 Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
 210 215 220
 Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
 225 230 235 240
 Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
 245 250 255
 Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
 260 265 270
 Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
 275 280 285
 Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
 290 295 300
 Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
 305 310 315 320
 Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu

200	205	210	
cag gcg ctg aaa gat gat gaa aat aac gag aac agt gat cat gac atg Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn Ser Asp His Asp Met 215 220 225			787
ggc gga gac atc att ccg tac ttc gtc tct cgc aat gat gcg cat gtt Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg Asn Asp Ala His Val 230 235 240 245			835
tat gat ttc tcc gga aac att gtt cct ggc gca act gag cgt gac aag Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala Thr Glu Arg Asp Lys 250 255 260			883
ggc tac tgg cgc gac gtc ggt acc att gat gcg ttc tac gag tgc cac Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Phe Tyr Glu Cys His 265 270 275			931
atg gac ctg att tcc gtg cac cca atc ttc aat ctg tat aac tct gag Met Asp Leu Ile Ser Val His Pro Ile Phe Asn Leu Tyr Asn Ser Glu 280 285 290			979
tgg cca atc cac acg acc tct gaa ggt aac ttg cct ccg gct aag ttc Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu Pro Pro Ala Lys Phe 295 300 305			1027
gtt cgg ggc ggt atc gcg cag tcg tcg atg gtg tct tca ggt tcc atc Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val Ser Ser Gly Ser Ile 310 315 320 325			1075
att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val 330 335 340			1123
gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val 345 350 355			1171
cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn 360 365 370			1219
gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp 375 380 385			1267
gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys 390 395 400 405			1315
aac cag gta gtc taaacgggaa agggacctta aaa Asn Gln Val Val			1350

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<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

<221> CDS

<222> (101)..(1327)

<223> RXA02063

<400> 275

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                                         Met Val Lys Gly Val
                                         1 5
aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc 163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly
                        10 15 20
aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca 211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro
                        25 30 35
ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg 259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val
                        40 45 50
aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat 307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His
                        55 60 65
tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg 355
Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn Val Ser Gly Pro Thr
                        70 75 80 85
ggg cag tac att gct tct gtt cct gcg cag cag cgc ctg ggc aag cga 403
Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln Arg Leu Gly Lys Arg
                        90 95 100
tgg ttc act ggt tcc gcg gat gca att ttg cag tct ctg aac ttg atc 451
Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln Ser Leu Asn Leu Ile
                        105 110 115
tct gat gag aaa ccg gat tat gtc atc gtt ttc ggc gcg gac cac gtg 499
Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe Gly Ala Asp His Val
                        120 125 130
tat cgc atg gac cca agc cag atg cta gat gag cac att gca tct ggt 547
Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu His Ile Ala Ser Gly
                        135 140 145
cgc gcg gtg tct gtg gca ggt att cgc gtt cca cgt gag gaa gca act 595
Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro Arg Glu Glu Ala Thr
                        150 155 160 165
gcg ttt ggt tgc atc cag tcc gat gtc gac ggc aac ata acc gag ttc 643
Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly Asn Ile Thr Glu Phe
                        170 175 180
ttg gaa aag cca gct gac cct ccg gga acc cct gat gat cct gac atg 691
Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro Asp Asp Pro Asp Met
                        185 190 195
act tac gcg tcg atg ggt aac tac att ttc acc act gaa gcc ctg atc 739
Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr Thr Glu Ala Leu Ile

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<400> 294

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 20 25 30

Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser
 35 40 45

His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly
 50 55 60

Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro
 65 70 75 80

Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile
 85 90 95

Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser
 100 105 110

Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu
 115 120 125

Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu
 130 135 140

Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala
 145 150 155 160

Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser
 165 170 175

Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe
 180 185 190

Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val
 195 200 205

Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln
 210 215 220

Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val
 225 230 235 240

Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys
 245 250 255

Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu
 260 265 270

Glu Tyr Lys
 275

<210> 295

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

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 70 75 80 85
 aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt 403
 Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu
 90 95 100
 gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt 451
 Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly
 105 110 115
 aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa 499
 Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu
 120 125 130
 cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt 547
 Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu Val Ser His Ile Gly
 135 140 145
 ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg 595
 Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu
 150 155 160 165
 cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc 643
 Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg
 170 175 180
 att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att 691
 Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile
 185 190 195
 ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca 739
 Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala
 200 205 210
 ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa 787
 Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu
 215 220 225
 ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg 835
 Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg
 230 235 240 245
 gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat 883
 Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His
 250 255 260
 gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag 925
 Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys
 265 270 275
 taaaatgggc gtggcaattc gag 948

<210> 294

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

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Met Asp Ala Arg Gly
1 5

atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc 163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp Ala Glu Ala Leu Phe
10 15 20

atg cag ggc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat 211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp
25 30 35

ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg 259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met
40 45 50

ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt 307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly
55 60 65

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Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
 200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787
 Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
 215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835
 Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
 230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883
 Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
 250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931
 Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
 265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973
 Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp
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tagcaacaca tgagcaaata tgc 996

<210> 292

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<212> PRT

<213> Corynebacterium glutamicum

<400> 292

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 20 25 30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
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<222> (101)..(973)

<223> FRXA00013

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 Met Glu Gly Met Thr 5
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aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
 Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys 20
 10 15

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
 Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu 35
 25 30

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
 His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg 50
 40 45

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
 Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp 65
 55 60

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
 Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val 85
 70 75 80

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
 Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala 100
 90 95

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
 Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp 115
 105 110

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
 Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu 130
 120 125

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547
 Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly 145
 135 140

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
 Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly 165
 150 155 160

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
 Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala 180
 170 175

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691
 Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile 195
 185 190

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30
 Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45
 Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60
 Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80
 Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95
 Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110
 Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125
 Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140
 Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160
 Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
 165 170 175
 Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
 180 185 190
 His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
 195 200 205
 Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
 210 215 220
 Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
 225 230 235 240
 Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
 245 250 255
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 275 280 285
 Ala Leu Asp
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<210> 291

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

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ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu 120 125 130			499
gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly 135 140 145			547
gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly 150 155 160 165			595
atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala 170 175 180			643
ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile 185 190 195			691
gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro 200 205 210			739
gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile 215 220 225			787
gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp 230 235 240 245			835
gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gca tgc Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys 250 255 260			883
atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala 265 270 275			931
gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp 280 285 290			973
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<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Met Glu Gly Met Thr																		
1 5																		
aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa	163																	
Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys																		
10 15 20																		
acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag																		211
Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu																		
25 30 35																		
cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc	259																	
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg																		
40 45 50																		
atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat	307																	
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp																		
55 60 65																		
gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt	355																	
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val																		
70 75 80 85																		
ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg	403																	
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala																		

Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr
 310 315 320 325

ggc gca acc atc aac ctt gct gaa agc atc gag gtt taaccatgac 1121
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<210> 288

<211> 337

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 288

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 20 25 30

Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly
 35 40 45

Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile
 50 55 60

Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val
 65 70 75 80

Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met
 85 90 95

Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu
 100 105 110

Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly
 115 120 125

Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro
 130 135 140

Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp
 145 150 155 160

Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His
 165 170 175

Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu
 180 185 190

Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr
 195 200 205

Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala
 210 215 220

Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val
 225 230 235 240

gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca	355
Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala	
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gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag	403
Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu	
90 95 100	
gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg	451
Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu	
105 110 115	
cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc	499
Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg	
120 125 130	
gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc	547
Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser	
135 140 145	
gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct	595
Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro	
150 155 160 165	
cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg	643
Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu	
170 175 180	
tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct	691
Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala	
185 190 195	
gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc	739
Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr	
200 205 210	
gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa	787
Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu	
215 220 225	
gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc	835
Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe	
230 235 240 245	
gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg	883
Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met	
250 255 260	
act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat	931
Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp	
265 270 275	
acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc	979
Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val	
280 285 290	
gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca	1027
Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala	
295 300 305	
cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc	1075

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
 180 185 190
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
 195 200 205
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
 210 215 220
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
 225 230 235 240
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
 245 250 255
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
 260 265 270
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
 275 280 285
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
 290 295 300
 Val Glu Tyr Phe Arg Thr His
 305 310

<210> 287
 <211> 1134
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1111)
 <223> RXA01887

<400> 287
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 Met Ser Val Lys Leu
 1 5
 gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc 163
 Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile
 10 15 20
 aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act 211
 Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr
 25 30 35
 ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct 259
 Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser
 40 45 50
 aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att 307
 Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile
 55 60 65

acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc 883
 Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser
 250 255 260

aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc 931
 Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg
 265 270 275

agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct 979
 Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro
 280 285 290

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
 295 300 305

act cac taggggaaaa tccaccacaa atc 1056
 Thr His
 310

<210> 286
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 286
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 20 25 30

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 35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
 50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110

Val Arg Lys Val Val Phe Thr Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175

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acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc														163		
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile																
10					15					20						
aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc														211		
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg																
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ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg														259		
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gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac														307		
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His																
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Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His																
70					75					80			85			
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc														403		
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr																
90					95					100						
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc														451		
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val																
105					110					115						
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca														499		
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro																
120					125					130						
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc														547		
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser																
135					140					145						
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc														595		
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly																
150					155					160			165			
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Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln																
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gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt														691		
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu																
185					190					195						
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc														739		
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg																
200					205					210						
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Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu																
230					235					240			245			

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Glu	Ser	Val	Asp	Glu	Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr	50	55	60
Tyr	Ala	Arg	Asp	Leu	Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu	65	70	75
Gly	Val	Arg	Val	Arg	Leu	Val	His	Gly	Gly	Gly	Glu	Arg	Ala	Asp	Ser	85	90	95
Val	Trp	Ala	Gly	Leu	Gln	Ala	Ile	Ser	Leu	Asp	Asp	Ala	Thr	Pro	Asp	100	105	110
Ala	Ile	Val	Leu	Ile	His	Asp	Ser	Ala	Arg	Ala	Leu	Thr	Pro	Pro	Gly	115	120	125
Met	Ile	Ala	Arg	Val	Val	Arg	Lys	Val	His	Glu	Gly	Ala	Thr	Ala	Val	130	135	140
Ile	Pro	Val	Leu	Pro	Val	Ser	Asp	Thr	Ile	Lys	Arg	Val	Ser	Pro	Asp	145	150	155
Gly	Gly	Val	Val	Val	Asp	Thr	Pro	Asn	Arg	Ala	Glu	Leu	Arg	Ala	Val	165	170	175
Gln	Thr	Pro	Gln	Gly	Phe	Leu	Leu	Ser	Glu	Leu	Val	Ala	Ala	Asn	Glu	180	185	190
Lys	Phe	Phe	Ala	Asp	Pro	Asn	Pro	Gly	Phe	Ile	Pro	Thr	Asp	Asp	Ala	195	200	205
Ser	Leu	Met	Glu	Trp	Tyr	Gly	Ala	Asp	Val	Val	Cys	Val	Gln	Gly	Asp	210	215	220
Pro	Met	Ala	Phe	Lys	Val	Thr	Thr	Pro	Ile	Asp	Met	Met	Leu	Ala	Gln	225	230	235
Arg	Ile	Thr	Asp	Glu	Ala	Glu	Pro	Thr	Ile	Phe	Glu	Val	Pro	Gly	Asp	245	250	255

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<211> 1056
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(1033)  
<223> RXA00825
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                                     Met Arg Thr Val Val
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Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu	90	95	100	
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc				451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile	105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg				499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val	120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca				547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro	135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc				595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val	150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc				643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly	170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac				691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp	185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg				739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp	200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa				787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys	215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa				835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu	230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg				888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp	250	255		
tag				891

<210> 284

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Met	Ser	Ser	Thr	Arg	Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly
1				5					10					15	

Arg	Gly	Thr	Arg	Leu	Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu
			20					25					30		

Thr Ala Pro Lys Ser Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp
 165 170 175
 Asn Arg Val Val Asp Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly
 180 185 190
 Glu Leu Glu Ile Thr Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala
 195 200 205
 Leu Thr Val Gln Arg Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly
 210 215 220
 Thr Ile Asp Ser Met Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln
 225 230 235 240
 Lys Arg Thr Gly Asn Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg
 245 250 255
 Glu Gly Phe Ile Thr Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu
 260 265 270
 Lys Lys Ser Gly Tyr Gly Asn Tyr Leu Leu Arg Ala Leu
 275 280 285

<210> 283
 <211> 891
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(868)
 <223> RXA02666

<400> 283
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 tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115
 Met Ser Ser Thr Arg
 1 5
 atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163
 Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly Arg Gly Thr Arg Leu
 10 15 20
 ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211
 Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
 25 30 35
 tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259
 Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
 40 45 50
 atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307
 Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
 55 60 65
 ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355
 Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg

<220>

<221> CDS

<222> (1)..(576)

<223> RXN01332

<400> 295

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cac atc tct gcc att att gag ccc gac gca gca cgt gcc gct gca gct 48
His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
  1             5             10             15

gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct 96
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
          20             25             30

atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag 144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
          35             40             45

ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc 192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
          50             55             60

ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc 240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
          65             70             75             80

gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc 288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
          85             90             95

atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa 336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
          100             105             110

tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac 384
Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
          115             120             125

cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc 432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
          130             135             140

gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt 480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
          145             150             155             160

gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc 528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
          165             170             175

ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg 576
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
          180             185             190

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<210> 296

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
 1 5 10 15
 Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
 20 25 30
 Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
 35 40 45
 Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
 50 55 60
 Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
 65 70 75 80
 Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
 85 90 95
 Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
 100 105 110
 Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
 115 120 125
 Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
 130 135 140
 Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
 145 150 155 160
 Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
 165 170 175
 Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
 180 185 190

<210> 297

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(549)

<223> FRXA01332

<400> 297

gca gca cgt gcc gct gca gct gca gaa gac gcg ccg ggt gca cag gcc 48
 Ala Ala Arg Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
 1 5 10 15
 ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg 96
 Phe Thr Arg Ile Glu Asp Ala Ile Ala Asp Ala Val Asp Ala Val
 20 25 30
 ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca 144
 Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala

35	40	45	
cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat			192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp			
50	55	60	
tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag			240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys			
65	70	75	80
cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac			288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn			
	85	90	95
aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg			336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met			
	100	105	110
ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag			384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln			
	115	120	125
tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca			432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro			
	130	135	140
tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag			480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys			
	145	150	155
acc tcc tca ctg gcg cac tcc ggc ctc aag gaa cca atc ctg gtg atc			528
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile			
	165	170	175
atg gag ctc gaa aac ggc gtg			549
Met Glu Leu Glu Asn Gly Val			
	180		

<210> 298

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Ala Ala Arg Ala Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
1 5 10 15

Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val
20 25 30

Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala
35 40 45

Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp
50 55 60

Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys
65 70 75 80

Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn

	85		90		95
Asn Leu Arg	Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met				
	100		105		110
Leu Arg Gly	Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln				
	115		120		125
Ser Met Leu Ile Thr Asp	Ser Val Val His Glu Phe Asp Val Ile Pro				
	130		135		140
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys					
	145		150		155
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile					
	165		170		175
Met Glu Leu Glu Asn Gly Val					
	180				

<210> 299
 <211> 1128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1105)
 <223> RXA01632

<400> 299
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 cccctccac taactgatct ttgaaaggct gaaaaaactc atg act ctt cgt atc 115
 Met Thr Leu Arg Ile
 1 5
 gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att 163
 Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile
 10 15 20
 gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att 211
 Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile Ala Asp Pro Phe Ile
 25 30 35
 gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca 259
 Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala
 40 45 50
 tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc 307
 Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile
 55 60 65
 ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa 355
 Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu
 70 75 80 85
 cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa 403
 Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu
 90 95 100

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg	451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val	
105 110 115	
atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat	499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn	
120 125 130	
gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc	547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile	
135 140 145	
atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc	595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser	
150 155 160 165	
ggg gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt	643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg	
170 175 180	
ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt	691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val	
185 190 195	
ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc	739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val	
200 205 210	
acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc	787
Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg	
215 220 225	
cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag	835
His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys	
230 235 240 245	
ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac	883
Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His	
250 255 260	
aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc	931
Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu	
265 270 275	
gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa	979
Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln	
280 285 290	
gga atc cgc gac ggc caa ggc ttc tca cca aac ttc gag gac ggc gtc	1027
Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val	
295 300 305	
atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc	1075
Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly	
310 315 320 325	
cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg	1125
Arg Thr Val Thr Leu Asn Pro Ala Asn Val	
330 335	

cct

1128

<210> 300

<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Thr Leu Arg Ile Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val
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His Ala Ala Asn Ile Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile
 20 25 30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly
 35 40 45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile
 50 55 60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile
 65 70 75 80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile
 85 90 95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp
 100 105 110

Gly Ala Ser Lys Val Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser
 115 120 125

Phe Ala Ala Ile Asn Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu
 130 135 140

Glu Gln Leu Val Ile Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp
 145 150 155 160

Tyr Ile Ala Gly Ser Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp
 165 170 175

Leu Asp Met Ala Arg Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala
 180 185 190

Thr Gly Ala Asn Val Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr
 195 200 205

Asp Gln Val Ile Val Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn
 210 215 220

Ile Val Asn Ser Arg His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu
 225 230 235 240

Ala Phe Gly Ser Lys Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr
 245 250 255

Thr Val Arg Lys His Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile
 260 265 270

Phe Asn Phe Phe Leu Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu

275						280					285					
Ala	Thr	Phe	Ala	Gln	Gly	Ile	Arg	Asp	Gly	Gln	Gly	Phe	Ser	Pro	Asn	
290						295					300					
Phe	Glu	Asp	Gly	Val	Ile	Ala	Leu	Glu	Leu	Ala	Asn	Ala	Cys	Leu	Glu	
305						310					315					320
Ser	Ala	Gln	Thr	Gly	Arg	Thr	Val	Thr	Leu	Asn	Pro	Ala	Asn	Val		
325						330					335					

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<210> 301
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1183)  
<223> RXA01633
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gtttagtcaa cgtctagtta atgcctaagg agaaaacctc atg aaa aac atc acc 115																
Met Lys Asn Ile Thr 5																
atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac 163																
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn 20																
atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag 211																
Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu 35																
atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg 259																
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala 50																
gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac 307																
Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp Lys Leu Ile Glu Asp 65																
ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat 355																
Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp 85																
gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag 403																
Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys 100																
ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att 451																
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile 115																
gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag gcg cgt ttt gac 499																
Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Arg Phe Asp 130																

ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc	547
Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly	
135 140 145	
tgg ctt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg	595
Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro	
150 155 160 165	
gtg tcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg	643
Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu	
170 175 180	
cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag	691
His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu	
185 190 195	
gtg tac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc	739
Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val	
200 205 210	
ggt gac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc	787
Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr	
215 220 225	
ctc gcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt	835
Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val	
230 235 240 245	
cgc ctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat	883
Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp	
250 255 260	
gaa aag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc	931
Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr	
265 270 275	
ggc gaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag	979
Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys	
280 285 290	
aat gag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac	1027
Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn	
295 300 305	
cct tgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca	1075
Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ile Val Ala Asp Ala	
310 315 320 325	
gct cag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta	1123
Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val	
330 335 340	
cgg gaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg	1171
Arg Glu Ile Leu Glu Ser Ala Gln Pro Val Glu Val Arg Ala Leu	
345 350 355	
gtt cca tct gct taaaacctta ctgcttatct aaa	1206
Val Pro Ser Ala	
360	

<210> 302

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Met Lys Asn Ile Thr Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg
 1 5 10 15

Met His Val Ala Asn Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg
 20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala
 35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp
 50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr
 65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro
 85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn
 100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His
 115 120 125

Gln Arg Arg Phe Asp Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp
 130 135 140

Ala Gly Asp Leu Gly Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp
 145 150 155 160

Ala Phe Pro Pro Pro Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe
 165 170 175

Arg Asp Val Ser Leu His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly
 180 185 190

Gln Asp Ile Val Glu Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro
 195 200 205

Glu Ile Gly Ala Val Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr
 210 215 220

Leu Ala Asp Gly Thr Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly
 225 230 235 240

Ala Gly His Asp Val Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr
 245 250 255

Ile Val Gly Leu Asp Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly
 260 265 270

Ile Asp Phe Pro Thr Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe
 275 280 285

Ala Asp Ala Tyr Lys Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu

290 295 300

Gly Glu Arg Glu Asn Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala
 305 310 315 320

Ile Val Ala Asp Ala Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val
 325 330 335

Lys Ile Pro Thr Val Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val
 340 345 350

Glu Val Arg Ala Leu Val Pro Ser Ala
 355 360

<210> 303
 <211> 1146
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1123)
 <223> RXN01406

<400> 303
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ttcctcctct tagaaaccca ctcttgaaag gtataaaaac atg act att cga atc 115
 Met Thr Ile Arg Ile
 1 5

gga ctc gtt ggc tac ggt gtc ggc ggc agg ctc ttt cac acc cct tac 163
 Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu Phe His Thr Pro Tyr
 10 15 20

atc caa gct tct acg cac tgc gaa tta gta ggc gta gtt gct cgt tcc 211
 Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly Val Val Ala Arg Ser
 25 30 35

gaa ggc acc aaa gca gcc gtt gca gaa gat ctt cca gat gtt gcc atc 259
 Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu Pro Asp Val Ala Ile
 40 45 50

gtg gga tcg ctg aca gaa ctc ctc gaa ctg ggc gtc gat gca gtg gtg 307
 Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly Val Asp Ala Val Val
 55 60 65

atc tcc acc cct cca gcc acg cgc cgg gaa ctg gcc ttg gaa gca atc 355
 Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu Ala Leu Glu Ala Ile
 70 75 80 85

aac gca ggt gtc gca gtg gtt gcc gat aaa ccg ttt gca cca tca gcc 403
 Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro Phe Ala Pro Ser Ala
 90 95 100

gca gat gcc atg gaa ctt gtc gaa gcc gcc gaa aag gct gga gtg ctg 451
 Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu Lys Ala Gly Val Leu
 105 110 115

ctc aac gtc ttc cac aac agg cgc aac gac acc cac att gtc acg gca 499

Leu	Asn	Val	Phe	His	Asn	Arg	Arg	Asn	Asp	Thr	His	Ile	Val	Thr	Ala		
	120						125					130					
ctg	gga	atc	caa	gaa	gaa	ctt	ggt	gcg	atg	cgt	gga	ctg	gac	ctg	cga	547	
Leu	Gly	Ile	Gln	Glu	Glu	Leu	Gly	Ala	Met	Arg	Gly	Leu	Asp	Leu	Arg		
	135					140					145						
cta	gac	ctg	atc	gaa	cct	gat	tcc	ttg	gag	gca	ggt	cct	gaa	ggt	ggt	595	
Leu	Asp	Leu	Ile	Glu	Pro	Asp	Ser	Leu	Glu	Ala	Gly	Pro	Glu	Gly	Gly		
	150				155					160					165		
ttg	ctg	cg	gat	ctg	ggc	tca	cac	gta	gtc	gat	cag	acc	ctg	gtt	ctc	643	
Leu	Leu	Arg	Asp	Leu	Gly	Ser	His	Val	Val	Asp	Gln	Thr	Leu	Val	Leu		
				170					175					180			
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Met	Gly	Pro	Ala	Thr	Ser	Val	Thr	Ala	Gln	Leu	Gly	Ser	Ile	Asp	Leu		
			185					190						195			
cca	gaa	ggc	cca	acc	aac	gca	agg	ttc	cg	atc	gtg	ttg	gaa	cat	gaa	739	
Pro	Glu	Gly	Pro	Thr	Asn	Ala	Arg	Phe	Arg	Ile	Val	Leu	Glu	His	Glu		
		200					205					210					
tcg	ggc	gcc	gta	tcg	cac	att	tct	gcc	agc	aag	att	gac	cg	ttg	gag	787	
Ser	Gly	Ala	Val	Ser	His	Ile	Ser	Ala	Ser	Lys	Ile	Asp	Arg	Leu	Glu		
	215					220					225						
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Ser	Trp	Glu	Ile	Arg	Leu	Val	Gly	Glu	Arg	Gly	Ser	Tyr	Val	Ser	Asn		
	230				235					240					245		
tac	acc	gac	gtg	cag	acc	gtg	gcg	atc	aaa	cag	gga	ctt	cga	cca	acc	883	
Tyr	Thr	Asp	Val	Gln	Thr	Val	Ala	Ile	Lys	Gln	Gly	Leu	Arg	Pro	Thr		
				250					255					260			
aat	gac	cg	gaa	cac	tgg	ggc	tac	gaa	tcg	gag	gag	cg	tgg	ggc	acc	931	
Asn	Asp	Arg	Glu	His	Trp	Gly	Tyr	Glu	Ser	Glu	Glu	Arg	Trp	Gly	Thr		
			265				270						275				
ttg	gtt	acc	gat	gaa	ggc	tca	aag	gtg	att	cct	tca	gca	caa	ggc	gat	979	
Leu	Val	Thr	Asp	Glu	Gly	Ser	Lys	Val	Ile	Pro	Ser	Ala	Gln	Gly	Asp		
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Tyr	Thr	Arg	Phe	Tyr	Asp	Ala	Phe	Ala	Leu	Ala	Val	Glu	Asn	Gly	Gly		
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Ala	Gly	Pro	Val	Pro	Ala	Arg	Glu	Gly	Val	Ala	Val	Leu	Lys	Val	Leu		
	310				315					320					325		
gat	gct	gta	gcc	cag	agc	gct	gcg	gaa	aaa	cg	acc	att	gag	ttg	agc	1123	
Asp	Ala	Val	Ala	Gln	Ser	Ala	Ala	Glu	Lys	Arg	Thr	Ile	Glu	Leu	Ser		
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<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

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 Phe His Thr Pro Tyr Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly
 20 25 30
 Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu
 35 40 45
 Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly
 50 55 60
 Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu
 65 70 75 80
 Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro
 85 90 95
 Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu
 100 105 110
 Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr
 115 120 125
 His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg
 130 135 140
 Gly Leu Asp Leu Arg Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala
 145 150 155 160
 Gly Pro Glu Gly Gly Leu Leu Arg Asp Leu Gly Ser His Val Val Asp
 165 170 175
 Gln Thr Leu Val Leu Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu
 180 185 190
 Gly Ser Ile Asp Leu Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile
 195 200 205
 Val Leu Glu His Glu Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys
 210 215 220
 Ile Asp Arg Leu Glu Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly
 225 230 235 240
 Ser Tyr Val Ser Asn Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln
 245 250 255
 Gly Leu Arg Pro Thr Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu
 260 265 270
 Glu Arg Trp Gly Thr Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro
 275 280 285
 Ser Ala Gln Gly Asp Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala
 290 295 300
 Val Glu Asn Gly Gly Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala

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305              310              315              320
Val Leu Lys Val Leu Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg
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Thr Ile Glu Leu Ser
              340

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<211> 1200
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1177)
<223> RXN01630
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																				1												
att	gtt	gtt	ggc	ctg	cta	ggc	atc	acc	cac	ccg	cat	gcg	tcg	gcg	cgg	163																
Ile	Val	Val	Gly	Leu	Leu	Gly	Ile	Thr	His	Pro	His	Ala	Ser	Ala	Arg																	
																10				15											20	
gtg	cgt	gcc	ctc	cgt	gaa	att	gat	ggg	gta	gag	gtc	gtc	gcc	gcc	gcg	211																
Val	Arg	Ala	Leu	Arg	Glu	Ile	Asp	Gly	Val	Glu	Val	Val	Ala	Ala	Ala																	
																25				30											35	
gat	act	gat	tcc	cgc	ctc	cag	tac	ttc	acc	gac	aaa	tat	gat	gtt	gaa	259																
Asp	Thr	Asp	Ser	Arg	Leu	Gln	Tyr	Phe	Thr	Asp	Lys	Tyr	Asp	Val	Glu																	
																40				45											50	
ccc	cgc	gag	atc	gat	gac	gtc	ttg	aac	gac	gat	cgc	atc	aac	gcc	atc	307																
Pro	Arg	Glu	Ile	Asp	Asp	Val	Leu	Asn	Asp	Asp	Arg	Ile	Asn	Ala	Ile																	
																55				60											65	
atg	gtt	cac	tcc	aag	agc	aag	gac	atg	gtc	cct	cac	gcc	aag	cgc	gcg	355																
Met	Val	His	Ser	Lys	Ser	Lys	Asp	Met	Val	Pro	His	Ala	Lys	Arg	Ala																	
																70				75											80	85
ctc	gcg	gcc	gga	aaa	tcc	gtc	gtc	gtg	gag	aag	ccc	ggc	ggg	gga	aca	403																
Leu	Ala	Ala	Gly	Lys	Ser	Val	Val	Val	Glu	Lys	Pro	Gly	Gly	Gly	Thr																	
																90				95											100	
gtg	gcg	gat	ctt	gag	gag	ctc	ctg	gcc	ctc	aaa	gaa	gct	gcc	gat	cct	451																
Val	Ala	Asp	Leu	Glu	Glu	Leu	Leu	Ala	Leu	Lys	Glu	Ala	Ala	Asp	Pro																	
																105				110											115	
cag	cga	atc	gtg	cag	gtc	ggg	tac	aac	gtc	cgc	ctg	tct	gaa	tcg	gtt	499																
Gln	Arg	Ile	Val	Gln	Val	Gly	Tyr	Asn	Val	Arg	Leu	Ser	Glu	Ser	Val																	
																120				125											130	
cag	aga	ttt	aaa	gag	ctt	ctc	gac	gcc	ggc	ctc	atc	ggc	gaa	gtc	gtc	547																
Gln	Arg	Leu	Lys	Glu	Leu	Leu	Asp	Ala	Gly	Leu	Ile	Gly	Glu	Val	Val																	
																135				140											145	

agc gtg caa gca cgc ggc gcc gca aaa gta ggt gag cat atc acc gag 595
 Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu
 150 155 160 165

 cac ctc aac caa ccc gca gac atg ggc ggt gtg ttg tgg att ctt ggc 643
 His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly
 170 175 180

 tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc 691
 Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser
 185 190 195

 gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc 739
 Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser
 200 205 210

 cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc 787
 Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val
 215 220 225

 agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc 835
 Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser
 230 235 240 245

 cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc 883
 Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu
 250 255 260

 cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca 931
 Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro
 265 270 275

 cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct 979
 Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala
 280 285 290

 cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc 1027
 Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile
 295 300 305

 agc aac ttc cgc aca gaa atg cag ggc tgg gtg aat tcc att cgc act 1075
 Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr
 310 315 320 325

 gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc 1123
 Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg
 330 335 340

 att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta 1171
 Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val
 345 350 355

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 Asn Ile

<210> 306

<211> 359

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 306

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Met Ser Asp Gln Lys Ile Val Val Gly Leu Leu Gly Ile Thr His Pro
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His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
      20              25              30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
      35              40              45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
 50              55              60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65              70              75              80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
      85              90              95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
      100              105              110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
      115              120              125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
      130              135              140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
      145              150              155              160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
      165              170              175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
      180              185              190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
      195              200              205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
      210              215              220

Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
      225              230              235              240

Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
      245              250              255

Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
      260              265              270

Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
      275              280              285

Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
      290              295              300

Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val

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tcggtcgcgg	ccgttatctt	tttaagagga	gaaatttttag	atg	agc	acg	tcc	acc	115							
				Met	Ser	Thr	Ser	Thr								
				1				5								
atc	agg	gtt	gcc	att	gcc	gga	gtc	gga	aac	tgc	gcg	acc	tcc	ctc	att	163
Ile	Arg	Val	Ala	Ile	Ala	Gly	Val	Gly	Asn	Cys	Ala	Thr	Ser	Leu	Ile	
			10						15					20		
cag	ggt	gtg	gaa	tat	tac	cga	aat	gcg	gat	cct	tcc	gaa	act	gtc	ccg	211
Gln	Gly	Val	Glu	Tyr	Tyr	Arg	Asn	Ala	Asp	Pro	Ser	Glu	Thr	Val	Pro	
			25					30					35			
ggt	ttg	atg	cac	gtc	aaa	ttc	ggt	gat	tac	cac	gtt	ggc	gac	att	gaa	259
Gly	Leu	Met	His	Val	Lys	Phe	Gly	Asp	Tyr	His	Val	Gly	Asp	Ile	Glu	
		40					45					50				
ttc	gtg	gcc	gcg	ttc	gac	gtc	gac	gcc	gaa	aaa	gta	ggc	atc	gat	ctt	307
Phe	Val	Ala	Ala	Phe	Asp	Val	Asp	Ala	Glu	Lys	Val	Gly	Ile	Asp	Leu	
		55				60					65					
gcc	gac	gcc	acc	gag	gct	tca	caa	aac	tgc	act	atc	aaa	atc	gcc	gat	355
Ala	Asp	Ala	Thr	Glu	Ala	Ser	Gln	Asn	Cys	Thr	Ile	Lys	Ile	Ala	Asp	
		70			75					80					85	
gtc	cca	cag	acc	ggc	atc	aac	gtg	ctg	cgt	ggc	ccg	act	ctc	gac	ggc	403
Val	Pro	Gln	Thr	Gly	Ile	Asn	Val	Leu	Arg	Gly	Pro	Thr	Leu	Asp	Gly	
			90						95					100		
ctg	ggc	gat	cat	tac	cgc	gcg	acc	atc	gac	gag	tcc	acc	gcc	gag	cca	451
Leu	Gly	Asp	His	Tyr	Arg	Ala	Thr	Ile	Asp	Glu	Ser	Thr	Ala	Glu	Pro	
			105					110					115			
gtc	gac	gtt	gtc	cag	gcg	ctt	atc	gac	gca	aaa	gcc	gat	gtt	ttg	gtg	499
Val	Asp	Val	Val	Gln	Ala	Leu	Ile	Asp	Ala	Lys	Ala	Asp	Val	Leu	Val	
		120					125					130				

tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa	547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln	
135 140 145	
gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc	595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe	
150 155 160 165	
atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc	643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile	
170 175 180	
cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc	691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr	
185 190 195	
cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat	739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp	
200 205 210	
cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg	787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met	
215 220 225	
ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca	835
Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala	
230 235 240 245	
gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac	883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp	
250 255 260	
cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac	931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp	
265 270 275	
cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt	979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val	
280 285 290	
ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct	1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser	
295 300 305	
gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat	1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp	
310 315 320 325	
cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag	1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys	
330 335 340	
tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag	1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu	
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Ala Phe Ile Ile Glu Ala	
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<210> 308
 <211> 363
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 308

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Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
      20           25           30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
      35           40           45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
      50           55           60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
      65           70           75           80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
      85           90           95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
      100          105          110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
      115          120          125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
      130          135          140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
      145          150          155          160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
      165          170          175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
      180          185          190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
      195          200          205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
      210          215          220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
      225          230          235          240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
      245          250          255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
      260          265          270

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
      275          280          285

Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp

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290 295 300

Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala
 305 310 315 320

Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser
 325 330 335

Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala
 340 345 350

Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala
 355 360

<210> 309
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(772)
 <223> RXN03057

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 Leu Ala Ser Asp Leu
 1 5

ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163
 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
 10 15 20

aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211
 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
 25 30 35

gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259
 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
 40 45 50

gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307
 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
 55 60 65

ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
 70 75 80 85

gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
 90 95 100

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
 Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
 105 110 115

gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499

Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
 120 125 130
 gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
 135 140 145
 tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
 150 155 160 165
 ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180
 ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
 185 190 195
 tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
 200 205 210
 cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
 His Glu Ser Gly Val His Thr Ser Glu Val Ser
 215 220
 aca 795

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 310
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 Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
 20 25 30
 Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
 35 40 45
 Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60
 His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80
 Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95
 Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
 100 105 110
 Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
 115 120 125
 Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp

130	135	140
Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln		
145	150	155
Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
	165	170
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
	180	185
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
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His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
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		220

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 <223> FRXA02902

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 Leu Ala Ser Asp Leu
 1 5
 ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163
 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
 10 15 20
 aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211
 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
 25 30 35
 gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259
 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
 40 45 50
 gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307
 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
 55 60 65
 ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
 70 75 80 85
 gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
 90 95 100

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
 Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
 105 110 115
 gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499
 Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
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 gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
 135 140 145
 tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Ala His Ser Gly Gly
 150 155 160 165
 ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180
 ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
 185 190 195
 tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
 200 205 210
 cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
 His Glu Ser Gly Val His Thr Ser Glu Val Ser
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 aca 795

<210> 312

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

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Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
 20 25 30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr

100					105					110						
Gln	Asn	Arg	Tyr	Asn	Val	Ser	Ser	Gln	Glu	Leu	Arg	Arg	Leu	Leu	Asp	
115					120					125						
Ser	Gly	Asp	Leu	Gly	Ala	Ile	Asn	Gly	Ala	Tyr	Ser	Ser	Val	Val	Trp	
130					135					140						
Thr	Arg	Thr	Pro	Gly	Tyr	Tyr	Thr	Gln	Lys	Pro	Trp	Arg	Gly	Gln	Gln	
145					150					155					160	
Ala	His	Ser	Gly	Gly	Gly	Leu	Leu	Met	Asn	Gln	Ala	Ile	His	Thr	Leu	
165					170					175						
Asp	Leu	Leu	Gln	Trp	Phe	Leu	Gly	Lys	Ala	Thr	Glu	Val	Lys	Gly	Thr	
180					185					190						
Val	Ser	Thr	Asp	Lys	Tyr	Ala	Asp	Val	Ile	Asp	Val	Glu	Asp	Thr	Ala	
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 Met Lys Lys Lys Ile 5
 1 5
 gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa 163
 Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys 20
 10 15 20
 gac ctc tcc cgc gac cac att gtc tac gcc ttg ggc cga aat cca gag 211
 Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu 35
 25 30 35
 cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc 259
 His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser 50
 40 45 50
 gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa 307
 Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys 65
 55 60 65
 aac ctc gac cac gtg gat acg ctg gtg cac gcc gcg gcg gtg gcg cgt 355

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Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg
 70              75              80              85

gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt 403
Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu
          90              95              100

gat ctc aac gtc att gtc ccg gcc gag ttg agt cgc caa ctc ttg ccc 451
Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro
          105              110              115

gcc ctc cgc gcg gca tcc ggc tgc gtc atc tac atc aac tcc ggc gcc 499
Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr Ile Asn Ser Gly Ala
          120              125              130

ggc aac gga cca cac ccc ggc aac acc atc tac gcc gcc agc aaa cac 547
Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His
          135              140              145

gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac 595
Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn
          150              155              160              165

ggc atc cgc gtc agc act gtc agc ccc ggc ccc acc aac acc ccc atg 643
Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met
          170              175              180

ctg caa ggc ctc atg gac tca caa ggc acc aac ttc cgc cca gag atc 691
Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn Phe Arg Pro Glu Ile
          185              190              195

tac atc gaa cca aaa gaa atc gcc aac gca atc aga ttc gtg att gac 739
Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile Arg Phe Val Ile Asp
          200              205              210

gct ggc gaa acc acc cag atc acc aac gtg gac gta cga cca cgt atc 787
Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile
          215              220              225

gaa ctg gcg gac cgg aaa gat tagttctggg gggcttctg ggc 831
Glu Leu Ala Asp Arg Lys Asp
230              235

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<210> 314

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

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Ile Glu Ile Val Lys Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu
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Gly Arg Asn Pro Glu His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val
          35              40              45

Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly
          50              55              60

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Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala
65 70 75 80

Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu
85 90 95

Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser
100 105 110

Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr
115 120 125

Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr
130 135 140

Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys
145 150 155 160

Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro
165 170 175

Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn
180 185 190

Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile
195 200 205

Arg Phe Val Ile Asp Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp
210 215 220

Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp
225 230 235

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(985)
<223> RXN02654

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gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115
Met Ile Ser Leu Leu
1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
25 30 35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259

Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu	Lys	Gly	Arg	Lys	Ala		
	40						45					50					
ctt	att	act	ggg	ggc	gat	tct	ggg	att	gga	gct	gcc	gta	gca	atc	gct	307	
Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala	Ala	Val	Ala	Ile	Ala		
	55					60					65						
tat	gct	cgc	gag	ggg	gca	gat	gtt	gcg	atc	gct	tac	ttg	ccc	gaa	gaa	355	
Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu		
	70				75				80						85		
caa	gcc	gat	gct	gac	aga	gtg	ctc	caa	gca	atc	gag	gaa	aca	ggg	caa	403	
Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln		
				90					95					100			
aaa	gct	ttt	tct	ttc	cct	ggg	gat	ctc	cgt	gat	cca	gaa	tac	tgt	cgc	451	
Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg		
			105					110					115				
tcg	ctg	gtc	caa	gag	acg	gtg	aac	gct	tta	ggg	ggc	cta	gac	atc	ttg	499	
Ser	Leu	Val	Gln	Glu	Thr	Val	Asn	Ala	Leu	Gly	Gly	Leu	Asp	Ile	Leu		
		120					125					130					
gtc	aac	aac	gcg	tca	cgt	cag	gtg	tgg	gca	cct	ggg	ttg	acc	gaa	att	547	
Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile		
	135					140					145						
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggg	agt	595	
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser		
	150				155				160						165		
ttt	cgg	gtt	acc	aaa	gca	gct	ata	cct	cat	ctg	aag	ccc	gga	tca	tcg	643	
Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser		
				170				175						180			
ata	atc	ttt	aca	tcg	tcc	att	cag	gcg	tac	caa	cct	tcg	gaa	acc	ctc	691	
Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu		
			185					190					195				
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739	
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly		
		200				205						210					
ttg	gca	agt	agt	ctg	ata	ggc	gat	ggc	att	cgg	gta	aat	tct	gta	gcc	787	
Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala		
	215					220					225						
cca	ggg	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggg	cag	cca	caa	835	
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln		
	230				235				240					245			
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggg	883	
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly		
			250					255					260				
cac	cct	gtt	gag	ttg	gca	ggg	gcg	tac	gtt	ttt	ctc	gct	tct	gac	gaa	931	
His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe	Leu	Ala	Ser	Asp	Glu		
			265					270					275				
gcc	agc	tat	gtg	gta	gga	gaa	acc	ctg	gga	gtc	aca	ggg	ggg	acg	ccc	979	
Ala	Ser	Tyr	Val	Val	Gly	Glu	Thr	Leu	Gly	Val	Thr	Gly	Gly	Thr	Pro		

280 285 290

acc cca tagtcggtac aagcgggaatc act 1008

Thr Pro
295

<210> 316
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 316

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Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser
20 25 30

Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu
35 40 45

Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
50 55 60

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
65 70 75 80

Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
85 90 95

Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
100 105 110

Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
115 120 125

Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
130 135 140

Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
145 150 155 160

Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
165 170 175

Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
180 185 190

Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
195 200 205

Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
210 215 220

Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
225 230 235 240

His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
245 250 255

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
 260 265 270

Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
 275 280 285

Thr Gly Gly Thr Pro Thr Pro
 290 295

<210> 317

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(985)

<223> FRXA02654

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 Met Ile Ser Leu Leu
 1 5
 aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
 10 15 20
 cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
 25 30 35
 ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259
 Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala
 40 45 50
 ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307
 Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala
 55 60 65
 tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa 355
 Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu
 70 75 80 85
 caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa 403
 Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln
 90 95 100
 aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc 451
 Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg
 105 110 115
 tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg 499
 Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu
 120 125 130
 gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att 547
 Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile

135	140	145	
acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt			595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser			
150	155	160	165
ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg			643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser			
	170	175	180
ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc			691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu			
	185	190	195
ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc			739
Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn Asn Leu Ser Lys Gly			
	200	205	210
ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc			787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala			
	215	220	225
cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa			835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln			
	230	235	240
gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt			883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly			
	250	255	260
cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa			931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu			
	265	270	275
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc			979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro			
	280	285	290
acc cca tagtcggtac aagcggaatc act			1008
Thr Pro			
295			

<210> 318

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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Pro	Pro	Lys	Gln	Ser	Gln	Pro	Glu	Pro	Gly	Leu	Asp	Ile	Lys	Leu	Ser
			20					25					30		

Pro	Gln	Ala	Asp	Ile	Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu
		35					40					45			

Lys	Gly	Arg	Lys	Ala	Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala
	50					55					60				

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
 245 250 255
 Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
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 Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
 275 280 285
 Thr Gly Gly Thr Pro Thr Pro
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 <210> 319
 <211> 1605
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1582)
 <223> RXN01049

 <400> 319
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 aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115
 Met Gly Ser Ile Pro

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aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct	163																
Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala																	
10 15 20																	
atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc	211																
Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser																	
25 30 35																	
ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc	259																
Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr																	
40 45 50																	
acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag	307																
Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu																	
55 60 65																	
atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac	355																
Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn																	
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atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca	403																
Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser																	
90 95 100																	
tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc	451																
Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr																	
105 110 115																	
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Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu																	
120 125 130																	
atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc	547																
Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr																	
135 140 145																	
tcc tac cac cca tcg cgc ttg ctg tgg ctg aaa act gag ttc gag aaa	595																
Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys Thr Glu Phe Glu Lys																	
150 155 160 165																	
gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag tac gtc tac	643																
Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu Tyr Val Tyr																	
170 175 180																	
ttc aaa ctt gca ggc atc acc gga atg gct act tcg att gcc gcg tgg	691																
Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile Ala Ala Trp																	
185 190 195																	
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Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu Thr Ile Leu																	
200 205 210																	
gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc aga aac cct	787																
Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile Arg Asn Pro																	
215 220 225																	
gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag tgg aag cac	835																
Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys Trp Lys His																	
230 235 240 245																	

ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc	883
Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser	
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aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc	931
Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala	
265 270 275	
gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag	979
Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln	
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Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile	
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Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu	
310 315 320 325	
cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa	1123
Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu	
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Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg	
345 350 355	
tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag	1219
Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln	
360 365 370	
gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc	1267
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gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca	1315
Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala	
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gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca	1363
Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro	
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gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct	1411
Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro	
425 430 435	
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Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu	
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Glu Gln Leu Glu Pro Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr	
455 460 465	
acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt	1555
Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu	
470 475 480 485	

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 Phe Asp Ala Leu Tyr Leu Lys Leu Val
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1602

cgc

1605

<210> 320

<211> 494

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 320

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Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
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Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
 85 90 95

Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
 100 105 110

Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
 115 120 125

Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
 130 135 140

Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys
 145 150 155 160

Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile
 165 170 175

Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr
 180 185 190

Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu
 195 200 205

Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly
 210 215 220

Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp
 225 230 235 240

Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro
 245 250 255

452

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tac gtc tac ttc aaa ctt gca ggc atc acc gga atg gct act tcg att	211																
Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile																	
25 30 35																	
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Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu																	
40 45 50																	
act atc ttg gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc	307																
Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile																	
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aga aac cct gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag	355																
Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys																	
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tgg aag cac ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc	403																
Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly																	
90 95 100																	
tgg cct tcc aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca	451																
Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala																	
105 110 115																	
gtc gcc gcc gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt	499																
Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val																	
120 125 130																	
ccc gaa cag atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac	547																
Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp																	
135 140 145																	
cag tgc atc gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc	595																
Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr																	
150 155 160 165																	
tgg ctg gaa cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg	643																
Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu																	
170 175 180																	
atc cgc gaa ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc	691																
Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser																	
185 190 195																	
ggg gaa cgc tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc	739																
Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr																	
200 205 210																	
aac att cag gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc	787																
Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe																	
215 220 225																	
gaa gcc ctc gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa	835																
Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys																	
230 235 240 245																	

gcc ggc gca gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc 883
 Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr
 250 255 260

gac cac cca gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca 931
 Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro
 265 270 275

gtc atc cct ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt 979
 Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu
 280 285 290

atc gtc ctt gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca 1027
 Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro
 295 300 305

ttc ggc acg acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca 1075
 Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala
 310 315 320 325

aga gag ctt ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg 1121
 Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
 330 335

cagtggaacg cgc 1134

<210> 322
 <211> 337
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 322
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 20 25 30
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 35 40 45
 Gly Glu Leu Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala
 50 55 60
 Leu Phe Gly Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys
 65 70 75 80
 Val Val Asp Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His
 85 90 95
 Ala Ile Pro Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp
 100 105 110
 Ser Lys Thr Val Ala Val Ala Ala Thr Ser Gly Ala Met Arg Val
 115 120 125
 Ile Leu Pro Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr
 130 135 140

Arg Val Ser Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val
 145 150 155 160
 Gly Arg Ala Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn
 165 170 175
 Leu Asp Glu Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val
 180 185 190
 Leu Pro Phe Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala
 195 200 205
 Gln Ala Thr Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu
 210 215 220
 Trp Arg Gly Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp
 225 230 235 240
 Glu His Met Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser
 245 250 255
 Gly Arg Val Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp
 260 265 270
 Ala Leu Asp Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu
 275 280 285
 Arg Gly Thr Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr
 290 295 300
 Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His
 305 310 315 320
 His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu
 325 330 335
 Val

<210> 323
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(574)
 <223> FRXA01050

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 Met Gly Ser Ile Pro 5
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 aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala
 10 15 20

atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser
 25 30 35

 ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr
 40 45 50

 acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu
 55 60 65

 atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn
 70 75 80 85

 atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser
 90 95 100

 tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451
 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr
 105 110 115

 tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa 499
 Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu
 120 125 130

 atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc 547
 Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr
 135 140 145

 tcc tac cac cca tcg cgc ttg ctg tgg tgaaaaactga gttcgagaaa 594
 Ser Tyr His Pro Ser Arg Leu Leu Trp
 150 155

 gag 597

<210> 324

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
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 Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30

 Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

 Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

 Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

 Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp

	85		90		95
Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu	100		105		110
Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu	115		120		125
Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly	130		135		140
Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp	145		150		155

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<220>
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 <222> (101)..(1042)
 <223> RXA00202

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 Met Tyr Ala Arg Lys
 1 5
 ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163
 Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala
 10 15 20
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 Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp
 25 30 35
 ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg 259
 Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val
 40 45 50
 cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc 307
 Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr
 55 60 65
 ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag 355
 Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln
 70 75 80 85
 ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca 403
 Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro
 90 95 100
 act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct 451
 Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala
 105 110 115
 gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg 499

Asp Ile Pro Val Val Ala Val	Asp Arg Ser Ser Asn Gly Gly Glu Val	
120	125	130
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct	547	
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala		
135	140	145
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg	595	
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu		
150	155	160
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt	643	
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe		
	170	175
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag	691	
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln		
	185	190
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg	739	
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu		
	200	205
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag	787	
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu		
	215	220
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Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp		
	230	235
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt	883	
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val		
	250	255
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg	931	
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu		
	265	270
gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac	979	
Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp		
	280	285
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Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn		
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Val Ala Asp Phe Lys		
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<210> 326

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

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 Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45
 Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140
 Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
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 Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300
 Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

<210> 327

<211> 1077

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1054)

<223> RXN00872

<400> 327

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                                         Met Thr Asn Leu Thr
                                         1 5
agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr
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Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys
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Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His
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Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly
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Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr
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gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile
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Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala
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Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg
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Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro
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Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg
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cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca 643
His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro
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gaa gag gcc acc aag cag gcg gaa tgg gcg ttg cag cat tcc acg gtg 691
Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu Gln His Ser Thr Val
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gcg gtt ggc aac aag gaa gaa tgc gaa atc gca gtg ggc gag acc gag 739
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cca gag cgc gcg ggc cga gca ctg ttg gaa cgc ggt gtg gag ttg gcc 787
 Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg Gly Val Glu Leu Ala
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atc gtc aag cag gga cct aag ggt gtc atg gcg atg acc aag gac gaa 835
 Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala Met Thr Lys Asp Glu
 230 235 240 245

acc gta gaa gtt cct ccg ttc ttc gtc gat gtc atc aac ggt ctt ggt 883
 Thr Val Glu Val Pro Pro Phe Phe Val Asp Val Ile Asn Gly Leu Gly
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gcc ggc gat gca ttc ggc ggc gcg ctg tgc cac ggt ctg ctc tct gaa 931
 Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His Gly Leu Leu Ser Glu
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tgg ccg ttg gaa aag gtt ctc cgt ttt gcc aac acc gcg ggt gcg ctt 979
 Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn Thr Ala Gly Ala Leu
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gtg gcg tcc cgt ctt gaa tgc tcc acc gca atg cct act acc gat gag 1027
 Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met Pro Thr Thr Asp Glu
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gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta 1074
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tct 1077

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<211> 318

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

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Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
 35 40 45

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly
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Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
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Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
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Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr

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 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
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 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
 130 135 140
 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
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 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met
 165 170 175
 Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu
 180 185 190
 Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala
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 Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg
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 Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala
 225 230 235 240
 Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val
 245 250 255
 Ile Asn Gly Leu Gly Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His
 260 265 270
 Gly Leu Leu Ser Glu Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn
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<223> FRXA00872

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 Met Thr Asn Leu Thr
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agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
 Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr

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Tyr	Leu	Gly	Gly	Ser	Ala	Ala	Asn	Val	Ser	Val	Ala	Ala	Ala	Arg	His																								
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Phe	Pro	Pro	Asp	Asp	Phe	Pro	Leu	Tyr	Phe	Tyr	Arg	Glu	Pro	Lys	Ala																								
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Ser	Arg	Gly	Thr	His	Arg	Glu	Ile	Leu	Thr	Thr	Arg	Ala	Asn	Arg	Arg																								
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cac	acc	atc	ttt	gat	ctg	gac	tac	cga								622																							
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<212> PRT

<213> Corynebacterium glutamicum

<400> 330

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Ala	Ala	Ala	Arg	His	Gly	His	Asn	Ser	Ala	Leu	Leu	Ser	Arg	Val	Gly
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 Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
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 Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr
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 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
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 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
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 <222> (101)..(1744)
 <223> RXN00799

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 Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu Asp
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 Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met
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 Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro
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 Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys
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 Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro

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 Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly His
 360 365 370
 cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg tgg 1267
 Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met Trp
 375 380 385
 ggc gtg gag gaa ctc agc gag cca gaa cgc ttc gcc gca gca gtg cgt 1315
 Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Ala Val Arg
 390 395 400 405
 gca ggc acc gac att ttc tcc gac atg gct aac cca cgt cga ctg ctc 1363
 Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu Leu
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 gaa gca gtt gct gag gga cac ctt gat gag tca gag ctg aat cag cca 1411
 Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asn Gln Pro
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 Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu Asn
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 cca tat gtc tct gaa gat gaa gca gaa aag atc att ggt gcg cca gag 1507
 Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu
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 gtt tct gca ttg ggc aac aaa gca cag ctt gat tcc gtc acc ttg ctg 1555
 Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu Leu
 470 475 480 485
 cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct gaa 1603
 Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu
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 gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca act 1651
 Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr
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 aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt ggt 1699
 Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu Gly
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 gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1744
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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile
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Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly
 65 70 75 80

Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp
 85 90 95

Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu
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Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr
 115 120 125

Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr
 130 135 140

Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val
 145 150 155 160

Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe
 165 170 175

Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu
 180 185 190

Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr
 195 200 205

Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly
 210 215 220

Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly
 225 230 235 240

Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val
 245 250 255

Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr
 260 265 270

Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp
 275 280 285

Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala
 290 295 300

Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly
 305 310 315 320

Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala
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 Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu
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 Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg
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 Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile
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 Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe
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 405 410 415
 Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser
 420 425 430
 Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu
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 Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile
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 Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp
 465 470 475 480
 Ser Val Thr Leu Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser
 485 490 495
 Cys Ser Lys Pro Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp
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<211> 1607

<212> DNA

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<222> (1)..(1584)

<223> FRXA00799

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Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg	
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Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr	
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ccc gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa	192
Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu	
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aag tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac	240
Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn	
65 70 75 80	
ccg atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc	288
Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser	
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Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg	
100 105 110	
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Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln	
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Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser	
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Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu	
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Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala	
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ctt cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa	576
Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys	
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Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp	
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ctc gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag	672
Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu	
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Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Val Val Arg Gly Leu	
225 230 235 240	
cag ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac	768
Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His	
245 250 255	
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Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His		
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Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr		
		275					280					285					
cat	ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	912	
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Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe		
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His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met		
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tgg	ggc	gtg	gag	gaa	ctc	agc	gag	cca	gaa	cgc	ttc	gcc	gca	gca	gtg	1152	
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val		
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Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu		
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ctc	gaa	gca	gtt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	1248	
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln		
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cca	gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggt	ctg	ttt	gag	1296	
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu		
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Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro		
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Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu		
	450					455					460						
ctg	cgt	aac	aac	ccc	atc	cgt	gct	gcc	act	gga	tcc	tgc	agc	aag	cct	1440	
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro		
465					470					475					480		
gaa	gat	cta	ccc	att	ggt	tac	tgg	ccg	tac	caa	gat	cga	cga	ggt	tca	1488	
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser		
				485				490						495			
act	aca	gct	gga	agc	agc	cat	tcg	cgc	aga	act	ccc	agg	ggt	aac	ctt	1536	
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu		

500	505	510	
ggt gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc			1584
Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro			
515	520	525	

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<211> 528

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

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Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg
20 25 30

Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr
35 40 45

Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu
50 55 60

Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn
65 70 75 80

Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser
85 90 95

Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg
100 105 110

Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln
115 120 125

Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser
130 135 140

Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu
145 150 155 160

Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala
165 170 175

Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys
180 185 190

Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp
195 200 205

Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu
210 215 220

Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu
225 230 235 240

Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His

245								250				255			
Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His
			260					265					270		
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr
		275					280					285			
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile
	290					295					300				
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp
305					310					315					320
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe
				325					330					335	
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly
			340					345					350		
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met
		355					360					365			
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val
	370					375					380				
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu
385					390					395					400
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln
				405					410					415	
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu
			420					425					430		
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro
		435				440						445			
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu
	450					455					460				
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro
465					470					475					480
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser
				485					490					495	
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu
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Gly	Val	Phe	Arg	Val	Arg	Ser	Arg	Ser	Cys	Asn	Arg	Val	Gly	Ser	Pro
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<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (101)..(1609)

<223> RXA00032

<400> 335

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				Met	Asn	Thr	Pro	Leu	
				1				5	

cag	ctc	aac	act	gaa	aac	ctg	cag	gaa	atc	gct	tcg	act	tcc	gga	gtg	163
Gln	Leu	Asn	Thr	Glu	Asn	Leu	Gln	Glu	Ile	Ala	Ser	Thr	Ser	Gly	Val	
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cag	atc	cca	gcg	ttc	aac	cgc	gct	gac	gtc	gcc	ccg	ggc	att	gtc	cac	211
Gln	Ile	Pro	Ala	Phe	Asn	Arg	Ala	Asp	Val	Ala	Pro	Gly	Ile	Val	His	
			25					30					35			

ttc	ggt	gtt	ggc	gga	ttc	cat	cgc	gct	cac	caa	gcg	atg	tac	ctc	aat	259
Phe	Gly	Val	Gly	Gly	Phe	His	Arg	Ala	His	Gln	Ala	Met	Tyr	Leu	Asn	
		40					45					50				

gaa	ttg	atg	aat	gag	ggc	aag	gcc	ttg	gat	tgg	ggc	atc	atc	ggc	atg	307
Glu	Leu	Met	Asn	Glu	Gly	Lys	Ala	Leu	Asp	Trp	Gly	Ile	Ile	Gly	Met	
	55					60					65					

ggt	gtc	atg	cct	tcc	gat	gtg	cgc	atg	cgc	gat	gcc	ctg	gcc	agc	caa	355
Gly	Val	Met	Pro	Ser	Asp	Val	Arg	Met	Arg	Asp	Ala	Leu	Ala	Ser	Gln	
	70				75					80					85	

gat	cac	ctt	tat	acc	ctg	acc	act	aaa	gct	cct	gat	gga	act	ctt	gat	403
Asp	His	Leu	Tyr	Thr	Leu	Thr	Thr	Lys	Ala	Pro	Asp	Gly	Thr	Leu	Asp	
				90					95					100		

caa	aaa	atc	atc	gga	tcc	atc	att	gac	tac	gtg	ttc	gct	ccc	gag	gac	451
Gln	Lys	Ile	Ile	Gly	Ser	Ile	Ile	Asp	Tyr	Val	Phe	Ala	Pro	Glu	Asp	
			105					110					115			

cca	gca	cgg	gcc	gtt	gca	acc	ctc	gcg	cag	gac	tcc	atc	cgc	att	gtt	499
Pro	Ala	Arg	Ala	Val	Ala	Thr	Leu	Ala	Gln	Asp	Ser	Ile	Arg	Ile	Val	
		120					125					130				

tcc	ctc	acg	gtg	act	gaa	ggc	gga	tac	aac	atc	gat	ccg	gcg	aca	gaa	547
Ser	Leu	Thr	Val	Thr	Glu	Gly	Gly	Tyr	Asn	Ile	Asp	Pro	Ala	Thr	Glu	
	135					140					145					

gat	ttc	gac	cac	acc	aac	cct	cga	atc	gtt	gct	gac	cgc	gaa	gcc	ctg	595
Asp	Phe	Asp	His	Thr	Asn	Pro	Arg	Ile	Val	Ala	Asp	Arg	Glu	Ala	Leu	
	150				155					160					165	

cag	gcg	ggc	gat	act	tcc	act	ttg	cag	acc	ttc	ttt	ggg	ttg	atc	act	643
Gln	Ala	Gly	Asp	Thr	Ser	Thr	Leu	Gln	Thr	Phe	Phe	Gly	Leu	Ile	Thr	
				170				175						180		

gcc	gca	ttg	att	tcc	cga	aaa	gaa	tca	gga	tct	acg	cca	ttt	acc	atc	691
Ala	Ala	Leu	Ile	Ser	Arg	Lys	Glu	Ser	Gly	Ser	Thr	Pro	Phe	Thr	Ile	
			185					190					195			

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Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp Leu Ala Lys Arg Phe	
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ttc ctc gcc ttc gca cat tcc gtg tct tct gag ctc ggc gaa tgg gtg	787
Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu Leu Gly Glu Trp Val	
215 220 225	
gaa aac aac gtg gcc ttc ccc aac tcc atg gtg gac cgc atc acc cct	835
Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val Asp Arg Ile Thr Pro	
230 235 240 245	
gaa acc acc gac ggc gac cgc gat gac atc aag gaa atc ggc tac atc	883
Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys Glu Ile Gly Tyr Ile	
250 255 260	
gat gcg tgg cca gtg gtt tct gaa gat ttc acc caa tgg gtc ctc gag	931
Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu	
265 270 275	
gat gcc ttc acc cag ggc cgc ccc gcg tac gag gag gtt ggc gtg cag	979
Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln	
280 285 290	
gtc gtc tcc gac gtg gag cct tat gaa tta atg aag ctg cgc ctg ctc	1027
Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu	
295 300 305	
aac gcc tcc cac cag gga ctt tgc tac ttc ggc cac ttg gct ggc cac	1075
Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly His Leu Ala Gly His	
310 315 320 325	
cac atg gtc cac gac gtc atg gcg gat acc cgc ttc cag gat ttc ctc	1123
His Met Val His Asp Val Met Ala Asp Thr Arg Phe Gln Asp Phe Leu	
330 335 340	
ctg gct tac atg gag cgc gaa gcc acc cct acc ctc aag gaa ctt cca	1171
Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr Leu Lys Glu Leu Pro	
345 350 355	
ggt gtc gat cta gat gct tat cga cgc caa ctc atc gcg cga ttc ggc	1219
Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly	
360 365 370	
aac gcc gca gtc aaa gac acc gta ccg cgc ctg tgt gcg gaa tcc tcc	1267
Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu Cys Ala Glu Ser Ser	
375 380 385	
gac cgc att cca aag tgg ctg ttg cca gtc gta cgc gaa aac ctc gca	1315
Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val Arg Glu Asn Leu Ala	
390 395 400 405	
gca ggc cgc gac gtc aca ctt tct gca gcc atc gtc gca tcc tgg gcg	1363
Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala	
410 415 420	
cgc tac gca gaa ggc acc gac gag cag ggc aac cca ata aag att gtt	1411
Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val	
425 430 435	
gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc	1459

Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr
 440 445 450
 gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc 1507
 Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val
 455 460 465
 gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt 1555
 Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu
 470 475 480 485
 cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta 1603
 His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val
 490 495 500
 act gtc taaatccgtt gcgcgctagg gtt 1632
 Thr Val

<210> 336
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 336
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 Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln
 35 40 45
 Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp
 50 55 60
 Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp
 65 70 75 80
 Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro
 85 90 95
 Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val
 100 105 110
 Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp
 115 120 125
 Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile
 130 135 140
 Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala
 145 150 155 160
 Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe
 165 170 175
 Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser
 180 185 190

Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp
 195 200 205
 Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu
 210 215 220
 Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val
 225 230 235 240
 Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys
 245 250 255
 Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr
 260 265 270
 Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu
 275 280 285
 Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met
 290 295 300
 Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly
 305 310 315 320
 His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg
 325 330 335
 Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr
 340 345 350
 Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu
 355 360 365
 Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu
 370 375 380
 Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val
 385 390 395 400
 Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile
 405 410 415
 Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn
 420 425 430
 Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala
 435 440 445
 Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile
 450 455 460
 Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu
 465 470 475 480
 Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala
 485 490 495
 Leu Leu Thr Gln Val Thr Val
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gactctggta atcgaaaatt aaaggtaagg ggggtgtggag					atg	tca	gca	aaa	tcg								115
					Met	Ser	Ala	Lys	Ser								
					1								5				
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Ser	Leu	Lys	Glu	Val	Ala	Glu	Leu	Ala	Gly	Val	Gly	Tyr	Ala	Thr	Ala		
					10						15						
tcg	agg	gca	cta	tct	ggc	aag	ggg	tat	gtg	tcc	ccg	cag	acg	cgg	gag	211	
Ser	Arg	Ala	Leu	Ser	Gly	Lys	Gly	Tyr	Val	Ser	Pro	Gln	Thr	Arg	Glu		
					25						30						
aaa	gtt	cag	gcg	gcg	gct	aaa	gag	ctg	aac	tat	gta	cca	aat	cag	ctg	259	
Lys	Val	Gln	Ala	Ala	Ala	Lys	Glu	Leu	Asn	Tyr	Val	Pro	Asn	Gln	Leu		
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gcc	aag	gcg	ttg	cgg	gaa	cat	cgc	agt	gcc	ttg	gtg	ggg	gtc	att	gtt	307	
Ala	Lys	Ala	Leu	Arg	Glu	His	Arg	Ser	Ala	Leu	Val	Gly	Val	Ile	Val		
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Pro	Asp	Leu	Ser	Asn	Glu	Tyr	Tyr	Ser	Glu	Ser	Leu	Gln	Thr	Ile	Gln		
					70						75						
cag	gat	ctg	aaa	gct	gct	ggc	tat	caa	atg	ctg	ggt	gcg	gag	gcc	aac	403	
Gln	Asp	Leu	Lys	Ala	Ala	Gly	Tyr	Gln	Met	Leu	Val	Ala	Glu	Ala	Asn		
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agt	gtg	cag	gcg	cag	gac	gtg	gtg	atg	gaa	tcg	ttg	atc	tcg	att	caa	451	
Ser	Val	Gln	Ala	Gln	Asp	Val	Val	Met	Glu	Ser	Leu	Ile	Ser	Ile	Gln		
					105						110						
gct	gca	gga	att	atc	cac	gtt	cca	gtg	gtc	ggc	tca	att	gct	cct	gaa	499	
Ala	Ala	Gly	Ile	Ile	His	Val	Pro	Val	Val	Gly	Ser	Ile	Ala	Pro	Glu		
					120						125						
gga	atc	ccc	atg	gtg	cag	ttg	act	cgt	ggt	gaa	ttg	ggt	cct	ggt	ttc	547	
Gly	Ile	Pro	Met	Val	Gln	Leu	Thr	Arg	Gly	Glu	Leu	Gly	Pro	Gly	Phe		
					135						140						
cct	cgg	gtg	ttg	tgt	gat	gat	gag	gct	ggg	ttt	ttt	cag	ctg	acc	gag	595	
Pro	Arg	Val	Leu	Cys	Asp	Asp	Glu	Ala	Gly	Phe	Phe	Gln	Leu	Thr	Glu		
					150						155						
tcg	gtg	ctg	ggc	ggc	agc	gga	atg	aac	att	gct	gct	ttg	gtt	ggt	gaa	643	
Ser	Val	Leu	Gly	Gly	Ser	Gly	Met	Asn	Ile	Ala	Ala	Leu	Val	Gly	Glu		
					170						175						

gaa tca ctt tcc acc acg cag gaa cga atg cgc ggt att agt cat gcg 691
 Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg Gly Ile Ser His Ala
 185 190 195
 gcg tcg ata tat ggg gct gag gtg acg ttc cat ttt ggc cac tat tct 739
 Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His Phe Gly His Tyr Ser
 200 205 210
 gtc gaa tct ggc gaa gag atg gct cag gtg gtg ttt aac aac ggc ctt 787
 Val Glu Ser Gly Glu Glu Met Ala Gln Val Val Phe Asn Asn Gly Leu
 215 220 225
 ccc gat gca ttg att gtg gcg tct cct cgg ctg atg gct ggg gtg atg 835
 Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu Met Ala Gly Val Met
 230 235 240 245
 cgt gct ttt act cgc ctg aat gtc cgc gtt ccc cac gat gtg gtg att 883
 Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro His Asp Val Val Ile
 250 255 260
 ggt ggt tat gac gat cct gag tgg tac agc ttt gtc ggc gcg ggg att 931
 Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe Val Gly Ala Gly Ile
 265 270 275
 acc acg ttt gtt cca ccg cat gag gag atg ggg aaa gag gcc gtg cgc 979
 Thr Thr Phe Val Pro Pro His Glu Glu Met Gly Lys Glu Ala Val Arg
 280 285 290
 ttg ttg gta gat ctg att gaa aat ccc gaa ctt ccc acc ggc gat gtg 1027
 Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu Pro Thr Gly Asp Val
 295 300 305
 gtt ttg cag ggg cag gtg atc ctt cgg ggg tcg agc aca cat tcc ggg 1075
 Val Leu Gln Gly Gln Ile Leu Arg Gly Ser Ser Thr His Ser Gly
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 tagaattgcc caaatgtcat caa 1098

<210> 338
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 338
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 Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr
 35 40 45
 Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu
 50 55 60
 Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser
 65 70 75 80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu
 85 90 95
 Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser
 100 105 110
 Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly
 115 120 125
 Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu
 130 135 140
 Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe
 145 150 155 160
 Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala
 165 170 175
 Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg
 180 185 190
 Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His
 195 200 205
 Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val
 210 215 220
 Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu
 225 230 235 240
 Met Ala Gly Val Met Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro
 245 250 255
 His Asp Val Val Ile Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe
 260 265 270
 Val Gly Ala Gly Ile Thr Thr Phe Val Pro Pro His Glu Glu Met Gly
 275 280 285
 Lys Glu Ala Val Arg Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu
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 Pro Thr Gly Asp Val Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser
 305 310 315 320
 Ser Thr His Ser Gly
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<210> 339

<211> 1246

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1246)

<223> RXN00316

<400> 339

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Met Gly Gln Cys Thr
1 5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
10 15 20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
25 30 35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
40 45 50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu
55 60 65

gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr
70 75 80 85

att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag 403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln
90 95 100

gtg atg gga aca aag ggt gcc acc atg acg atc ctg gaa ttc cct gaa 451
Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile Leu Glu Phe Pro Glu
105 110 115

ggt acc gac ggc agg ctc att gtt cgc agt gaa aac gac acc cgt cga 499
Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu Asn Asp Thr Arg Arg
120 125 130

aac cac ccc att cca ccc cgc gga tct tta tcc caa tgc cga tct ttc 547
Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser Gln Cys Arg Ser Phe
135 140 145

cat cat caa cgg tgc ttt gat ccc gta tca cac cgc cca gat cgc aga 595
His His Gln Arg Cys Phe Asp Pro Val Ser His Arg Pro Asp Arg Arg
150 155 160 165

ctt tat cga tgc gct caa cga agg ccg ccc acc act gat cac cgg ccg 643
Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr Thr Asp His Arg Pro
170 175 180

cga tgc cac cag agc tct gaa agt tct cct tgg tgt cta cga atc agc 691
Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp Cys Leu Arg Ile Ser
185 190 195

agc cac cca cca gcc ggt ctc ttt gat cta acg gaa gct ttt aaa acg 739
Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr Glu Ala Phe Lys Thr
200 205 210

tca cgc caa atc ggt ctt gca cct tta tcc tcc ctg tcc aca cca cct 787
Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser Leu Ser Thr Pro Pro
215 220 225

gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt 835
Asp Gln Leu Val Arg Leu Ala Ala Thr Gly Phe Ser Phe Val Gly
230 235 240 245

ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc 883
Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser
250 255 260

cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc 931
Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr
265 270 275

gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc 979
Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr
280 285 290

acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga 1027
Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly
295 300 305

gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg 1075
Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu
310 315 320 325

acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc 1123
Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val
330 335 340

acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg 1171
Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro
345 350 355

cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac 1219
Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp
360 365 370

acc ttg cac atg gcc agg ttc gga gcc 1246
Thr Leu His Met Ala Arg Phe Gly Ala
375 380

<210> 340

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
1 5 10 15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
 85 90 95
 Gly Ala Gln Val Gln Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile
 100 105 110
 Leu Glu Phe Pro Glu Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu
 115 120 125
 Asn Asp Thr Arg Arg Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser
 130 135 140
 Gln Cys Arg Ser Phe His His Gln Arg Cys Phe Asp Pro Val Ser His
 145 150 155 160
 Arg Pro Asp Arg Arg Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr
 165 170 175
 Thr Asp His Arg Pro Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp
 180 185 190
 Cys Leu Arg Ile Ser Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr
 195 200 205
 Glu Ala Phe Lys Thr Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser
 210 215 220
 Leu Ser Thr Pro Pro Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly
 225 230 235 240
 Phe Ser Phe Val Gly Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg
 245 250 255
 Val Tyr Asp Leu Ser Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln
 260 265 270
 Ala Leu Lys Glu Thr Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln
 275 280 285
 Val Asn Ala Asp Thr Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala
 290 295 300
 Ala Gly Ala Leu Gly Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp
 305 310 315 320
 Asn Ile Ala Pro Leu Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala
 325 330 335
 Arg Asp Phe Gly Val Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser
 340 345 350
 Val His Ser Ile Pro Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly
 355 360 365
 Lys Val Val Ala Asp Thr Leu His Met Ala Arg Phe Gly Ala
 370 375 380

<210> 341

<211> 412

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(412)

<223> FRXA00309

<400> 341

agcgcatgat cgatgcctgc gagtccgcag gggccaact tggcgtgctc ttccagcgcc 60

gcttctggcc cgcggctcaa aaaatgaaaa aggagccgctc atg ggc caa tgc acg 115
 Met Gly Gln Cys Thr
 1 5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163
 Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
 10 15 20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211
 Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
 25 30 35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259
 His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
 40 45 50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307
 Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu
 55 60 65

gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355
 Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr
 70 75 80 85

att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag 403
 Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln
 90 95 100

gtg atg gga 412
 Val Met Gly

<210> 342

<211> 104

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
 1 5 10 15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
 20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
 35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
 50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
 65 70 75 80
 Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
 85 90 95
 Gly Ala Gln Val Gln Val Met Gly
 100

<210> 343
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> RXN00310

<400> 343
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 aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
 Met Ser Asp Lys Ile
 1 5
 tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163
 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
 10 15 20
 gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
 25 30 35
 gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
 40 45 50
 ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
 55 60 65
 gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70 75 80 85
 gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
 90 95 100
 gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
 105 110 115
 gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
 120 125 130
 aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545

Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145

ccgagagcat tcc

558

<210> 344
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 344
 Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
 1 5 10 15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
 130 135 140

Arg
 145

<210> 345
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> FRXA00310

<400> 345
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aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
 Met Ser Asp Lys Ile
 1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163

Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
 10 15 20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
 25 30 35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
 40 45 50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
 55 60 65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70 75 80 85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
 90 95 100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
 105 110 115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
 120 125 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545
 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145

ccgagagcat tcc 558

<210> 346

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
 1 5 10 15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
130 135 140

Arg
145

<210> 347

<211> 1342

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXA00041

<400> 347

atgaagcagc agcatccaag ctggaaaacg ctgatcacta ccgtctcatg gagcaattaa 60

agctgcgcta gaaacaaaaa ggaaagtagt gtgtggggct atg cac aca gaa ctt 115
Met His Thr Glu Leu
1 5

tcc agt ttg cgc cct gcg tac cat gtg act cct ccg cag ggc agg ctc 163
Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro Pro Gln Gly Arg Leu
10 15 20

aat gat ccc aac gga atg tac gtc gat ggc gat acc ctc cac gtc tac 211
Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp Thr Leu His Val Tyr
25 30 35

tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc tgg 259
Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly Trp
40 45 50

gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg acg 307
Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp Thr
55 60 65

cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat gga 355
His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp Gly
70 75 80 85

tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt ttc 403
Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu Phe
90 95 100

tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa aac 451
Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln Asn
105 110 115

ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat cgc 499
Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His Arg

120	125	130	
cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc aca Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe Thr 135 140 145			547
ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg aaa Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp Lys 150 155 160 165			595
atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt cta Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val Leu 170 175 180			643
tac cgc tcg aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc acc Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile Thr 185 190 195			691
ttt gac ctc agt gat gca caa cct ggt tct gct cct gat ctc gtt ccc Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala Pro Asp Leu Val Pro 200 205 210			739
ggt ggc tac atg tgg gaa tgc ccc aac ctt ttt acg ctt cgc gat gaa Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe Thr Leu Arg Asp Glu 215 220 225			787
gaa act ggc gaa gat ctc gac gtg ctg att ttc tgt cca caa gga ttg Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe Cys Pro Gln Gly Leu 230 235 240 245			835
gac cga atc cac gat gag gtt act cac tac gca agc tct gac cag tgc Asp Arg Ile His Asp Glu Val Thr His Tyr Ala Ser Ser Asp Gln Cys 250 255 260			883
gga tat gtc gtc ggc aag ctt gaa gga acg acc ttc cgc gtc ttg cga Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg 265 270 275			931
gga ttc agc gag ctg gat ttc ggc cat gaa ttc tac gca ccg cag gtt Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe Tyr Ala Pro Gln Val 280 285 290			979
gca gta aac ggt tct gat gcc tgg ctc gtg ggc tgg atg ggg ctg ccc Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly Trp Met Gly Leu Pro 295 300 305			1027
gcg cag gat gat cac cca aca gtt gca cgg gaa gga tgg gtg cac tgc Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu Gly Trp Val His Cys 310 315 320 325			1075
ctg act gtg ccc cgc aag ctt cat ttg cgc aac cac gcg atc tat caa Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn His Ala Ile Tyr Gln 330 335 340			1123
gag ctt ctt ctc cca gag ggg gag tca ggg gta atc aga tct gta tta Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val Ile Arg Ser Val Leu 345 350 355			1171
ggt tct gaa cct gtc cga gta gac atc cga ggc aat att tcc ctc gag Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly Asn Ile Ser Leu Glu 360 365 370			1219

tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta 1267
 Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val
 375 380 385

gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc 1315
 Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala
 390 395 400 405

att gag ata act gca ggt gat gga cag 1342
 Ile Glu Ile Thr Ala Gly Asp Gly Gln
 410

<210> 348

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
 1 5 10 15

Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
 20 25 30

Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
 35 40 45

Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
 50 55 60

Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser
 65 70 75 80

Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly
 85 90 95

Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg
 100 105 110

Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
 115 120 125

Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
 130 135 140

Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
 145 150 155 160

Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
 165 170 175

Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe
 180 185 190

Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala
 195 200 205

Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
 210 215 220

Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
 225 230 235 240
 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala
 245 250 255
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr
 260 265 270
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
 275 280 285
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
 290 295 300
 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu
 305 310 315 320
 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn
 325 330 335
 His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
 340 345 350
 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly
 355 360 365
 Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly
 370 375 380
 Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
 385 390 395 400
 Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln
 405 410

<210> 349

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(720)

<223> RXA02026

<400> 349

cca ttt cat ata caa cca gaa aca ggt tta tta aat gat ccc aac gga 48
 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15

ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96
 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat 144
 Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45

gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act 192
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60

aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac 240
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80

ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg 288
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95

caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca 336
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110

gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat 384
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125

aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat 432
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140

tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta 480
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160

ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata 528
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175

aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac 576
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
 180 185 190

ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att 624
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
 195 200 205

gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata 672
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
 210 215 220

ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt 720
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
 225 230 235 240

<210> 350

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15

Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
 180 185 190
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
 195 200 205
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
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 Met Thr Asn Val Ser
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 ggg tat cac cga cca gag ctg cac atc acc gct gaa agt ggt gtt ttg 163

Gly	Tyr	His	Arg	Pro	Glu	Leu	His	Ile	Thr	Ala	Glu	Ser	Gly	Val	Leu		
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Phe	Ala	Pro	Ala	Gly	Val	Leu	Leu	Asp	Asp	Asp	Thr	Trp	His	Phe	Phe		
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His	Gln	Tyr	Arg	Pro	Ser	Pro	Asp	His	Gly	Pro	Arg	Trp	Ala	His	Gln		
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Phe	Ala	Glu	Arg	Thr	Pro	Phe	Val	Trp	Asp	Ile	Cys	Asp	Asp	Val	Leu		
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Ala	Pro	Glu	Gly	Asp	Glu	Thr	Gln	Val	Arg	Ala	Gly	Ser	Val	Val	Ser		
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Asn	Asn	Gly	Gly	Val	Asp	Leu	Tyr	Phe	Thr	Ser	Val	Val	Gly	Pro	Thr		
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Gly	Glu	Val	Val	Gly	Asn	Thr	Asp	Gly	Tyr	Val	Lys	Phe	Arg	Ser	Pro		
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Cys	Val	Ile	Pro	Gly	Trp	Glu	Asp	Gln	Gly	Asn	Arg	Asp	Glu	Gly	His		
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Ser	Gly	Trp	Leu	Met	Leu	Ala	Val	Thr	Gly	Pro	Val	Glu	Ala	Pro	Thr		
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Val	Val	Val	Leu	Asp	Ser	Pro	Asp	Gly	Arg	Glu	Trp	Ser	Ile	Thr	Gly		
			185					190					195				
ccc	ctg	tct	ctc	aac	ggc	ctc	tct	gga	tta	gag	tca	gac	gaa	gtt	cta	739	
Pro	Leu	Ser	Leu	Asn	Gly	Leu	Ser	Gly	Leu	Glu	Ser	Asp	Glu	Val	Leu		
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Val	Ala	Pro	Arg	Met	Ile	Arg	Leu	Arg	Asp	Glu	Val	Asp	His	Glu	Ile		
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Tyr	Asp	Val	Leu	Ile	Val	Thr	Ile	Glu	Gln	Asp	Gly	Ile	Asp	Ile	Ser		
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Pro	Phe	Thr	Arg	Ile	Asp	Phe	Gly	His	Asp	Phe	Ser	Arg	Pro	Arg	Asn					
265					270					275										
acc	aac	tac	gcc	gaa	acc	acc	atc	ggc	tac	gac	ttc	gcc	cac	atc	ttt	979				
Thr	Asn	Tyr	Ala	Glu	Thr	Thr	Ile	Gly	Tyr	Asp	Phe	Ala	His	Ile	Phe					
280					285					290										
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Leu	Asp	Ala	Ile	His	Glu	Ser	Glu	Ala	Ala	Ala	Gly	Trp	Thr	Gly	Leu					
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Glu	Gly	Glu	Ile	Ala	Ala	Thr	Ile	Thr	His	Arg	His	Asn	Gln	Leu	Val					
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Val	Asp	Arg	Ser	Met	Asn	Pro	Asn	His	Ala	Gly	Asp	Pro	His	Ala	Ile					
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Ala	Pro	Leu	Thr	Asp	Asp	Glu	Thr	Asp	Ser	Leu	Phe	Ile	Val	Val	Asp					
410					415					420										
ggc	tct	aca	gta	gaa	gtt	ttt	gct	gat	ggc	ggt	tat	gta	tca	atg	gca	1411				
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425					430					435										
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Thr	Thr	Gly	Asp	Ala	Ser	Ile	Ile	Arg	Gln	Glu	Ser	His	Phe	Pro	Val					
455					460					465										
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Asp	Phe	Ser	Ser	Val	Ser	Leu	Asp	Ile	Asp	Asp	Leu	Thr	Ala	Leu	Met					
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1617

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<211> 498

<212> PRT

<213> Corynebacterium glutamicum

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Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
 35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile
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Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala
 65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser
 85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile
 100 105 110

Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro
 115 120 125

Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val
 130 135 140

Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn
 145 150 155 160

Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro
 165 170 175

Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu
 180 185 190

Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu
 195 200 205

Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu
 210 215 220

Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp
 225 230 235 240

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Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe
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                Met Glu Leu Leu Glu
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ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg	211															
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp																
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Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu																
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aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt	307															
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val																
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cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca	451															
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala																
105				110				115								
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt	499															
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val																
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gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac	547															
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn																
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Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr																
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Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu																
170				175				180								
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc	691															
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile																
185				190				195								
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt	739															
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg																
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gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa	787															
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu																
215				220				225								
cag tac ccc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg aac ttc	835															
Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe																
230				235				240				245				

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 Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu
 250 255 260

cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac 931
 His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp
 265 270 275

aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag 979
 Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu
 280 285 290

ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac 1027
 Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp
 295 300 305

gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa 1075
 Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu
 310 315 320 325

ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac 1123
 Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His
 330 335 340

gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa 1171
 Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu
 345 350 355

gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt 1219
 Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val
 360 365 370

cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta 1267
 Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val
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 Phe Leu Ala Arg Val
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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
 20 25 30
 Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
 35 40 45
 Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
 50 55 60
 Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu

65	70	75	80
Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro	85	90	95
Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly	100	105	110
Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys	115	120	125
Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe	130	135	140
Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu	145	150	155
Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu	165	170	175
Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys	180	185	190
Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu	195	200	205
Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile	210	215	220
Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala	225	230	235
Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu	245	250	255
Asp Ala Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile	260	265	270
Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr	275	280	285
Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu	290	295	300
Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro	305	310	315
Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu	325	330	335
Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly	340	345	350
Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly	355	360	365
His Ala Ala Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser	370	375	380
Glu Asp Ala Glu Val Phe Leu Ala Arg Val	385	390	

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 <223> FRXA01369

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 aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca 96
 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
 20 25 30
 aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac 144
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
 35 40 45
 tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc 192
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
 50 55 60
 ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc 240
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65 70 75 80
 gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc 288
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
 85 90 95
 aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc 336
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
 100 105 110
 aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc 384
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
 115 120 125
 ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca 432
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
 130 135 140
 tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca 480
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
 145 150 155 160
 gaa gta ttc ctc gct agg gtt tagatctttt tagattaaaa tca 524
 Glu Val Phe Leu Ala Arg Val
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<210> 356
 <211> 167
 <212> PRT

<213> Corynebacterium glutamicum

<400> 356

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Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
20 25 30

Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
35 40 45

Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
50 55 60

Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
65 70 75 80

Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
85 90 95

Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
100 105 110

Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
115 120 125

Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
130 135 140

Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
145 150 155 160

Glu Val Phe Leu Ala Arg Val
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<210> 357

<211> 808

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(808)

<223> FRXA01373

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Met Glu Leu Leu Glu
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ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp
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ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg 211
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp
25 30 35

ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc 259
 Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu
 40 45 50

aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt 307
 Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val
 55 60 65

gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca 355
 Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala
 70 75 80 85

gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc 403
 Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala
 90 95 100

cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca 451
 Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala
 105 110 115

ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt 499
 Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val
 120 125 130

gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac 547
 Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn
 135 140 145

acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac 595
 Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr
 150 155 160 165

cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg 643
 Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu
 170 175 180

ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc 691
 Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile
 185 190 195

gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt 739
 Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg
 200 205 210

gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa 787
 Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu
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cag tac ccc ggc gat gtc ggc 808
 Gln Tyr Pro Gly Asp Val Gly
 230 235

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<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg

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Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro	20	25	30
Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile	35	40	45
Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala	50	55	60
Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu	65	70	75
Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro	85	90	95
Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly	100	105	110
Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys	115	120	125
Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe	130	135	140
Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu	145	150	155
Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu	165	170	175
Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys	180	185	190
Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu	195	200	205
Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile	210	215	220
Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly	225	230	235

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aag att gag gcc ggc cag ggt tcg gat gag ttg tat aac gac ttt gag	96
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Lys	Ile	Glu	Ala	Gly	Gln	Gly	Ser	Asp	Glu	Leu	Tyr	Asn	Asp	Phe	Glu		
			20					25					30				
cac	ggg	gct	cag	ctg	ttt	gag	cgt	gct	gcg	gag	aat	ttg	tct	aaa	gag	144	
His	Gly	Ala	Gln	Leu	Phe	Glu	Arg	Ala	Ala	Glu	Asn	Leu	Ser	Lys	Glu		
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gat	agg	act	gcg	ctt	ttc	gac	gtc	gcc	tcc	tct	ctg	cgg	cgc	ggc	ggc	192	
Asp	Arg	Thr	Ala	Leu	Phe	Asp	Val	Ala	Ser	Ser	Leu	Arg	Arg	Gly	Gly		
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gat	gta	cgc	gca	cgt	ctc	gcc	cca	gcg	ctc	acc	gcg	agt	gtc	act	cat	240	
Asp	Val	Arg	Ala	Arg	Leu	Ala	Pro	Ala	Leu	Thr	Ala	Ser	Val	Thr	His		
	65				70					75					80		
ctt	tta	gaa	ctt	aac	ccg	ttg	cgt	gag	ttg	gtc	acg	atg	ggg	gaa	aac	288	
Leu	Leu	Glu	Leu	Asn	Pro	Leu	Arg	Glu	Leu	Val	Thr	Met	Gly	Glu	Asn		
				85					90					95			
ctg	cag	gtt	cgt	gtc	gag	cgt	cgt	gcc	gct	ttg	gtc	aac	tct	tgg	tat	336	
Leu	Gln	Val	Arg	Val	Glu	Arg	Arg	Ala	Ala	Leu	Val	Asn	Ser	Trp	Tyr		
			100					105					110				
gag	ctt	ttc	cct	cgt	tcc	aca	ggg	ggg	tgg	gat	gag	tcc	ggc	acc	ccc	384	
Glu	Leu	Phe	Pro	Arg	Ser	Thr	Gly	Gly	Trp	Asp	Glu	Ser	Gly	Thr	Pro		
		115					120					125					
gtt	cat	ggc	act	ttc	gct	acc	act	gct	cag	gcg	ttg	gag	cgt	gtc	gcg	432	
Val	His	Gly	Thr	Phe	Ala	Thr	Thr	Ala	Gln	Ala	Leu	Glu	Arg	Val	Ala		
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Lys	Met	Gly	Phe	Asp	Thr	Val	Tyr	Phe	Pro	Pro	Ile	His	Pro	Ile	Gly		
	145				150					155					160		
gag	gtc	aac	cgc	aag	ggc	cgc	aat	aat	acg	ctg	acc	ccg	gaa	cct	cat	528	
Glu	Val	Asn	Arg	Lys	Gly	Arg	Asn	Asn	Thr	Leu	Thr	Pro	Glu	Pro	His		
				165					170					175			
gat	gtg	ggg	tcg	ccg	tgg	gct	att	ggg	tct	aaa	gat	ggg	ggg	cat	gat	576	
Asp	Val	Gly	Ser	Pro	Trp	Ala	Ile	Gly	Ser	Lys	Asp	Gly	Gly	His	Asp		
			180					185					190				
gca	acg	cat	ccg	cgg	ttg	ggc	acc	att	gaa	gat	ttc	cag	gcg	ttg	ttg	624	
Ala	Thr	His	Pro	Arg	Leu	Gly	Thr	Ile	Glu	Asp	Phe	Gln	Ala	Leu	Leu		
		195					200					205					
gct	cgc	gca	cgg	gaa	ctc	aat	ttg	gaa	gtt	gca	ctc	gat	cta	gct	ctg	672	
Ala	Arg	Ala	Arg	Glu	Leu	Asn	Leu	Glu	Val	Ala	Leu	Asp	Leu	Ala	Leu		
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cag	gct	gcc	cct	gat	cat	cca	tgg	gcg	cag	gaa	cac	cgc	gag	ttt	ttc	720	
Gln	Ala	Ala	Pro	Asp	His	Pro	Trp	Ala	Gln	Glu	His	Arg	Glu	Phe	Phe		
	225				230					235					240		
acg	gtg	ttg	gct	gat	ggc	acc	att	gcg	tat	gca	gaa	aac	cca	ccg	aag	768	
Thr	Val	Leu	Ala	Asp	Gly	Thr	Ile	Ala	Tyr	Ala	Glu	Asn	Pro	Pro	Lys		
				245				250					255				
aag	tac	cag	gat	att	tat	ccc	atc	aac	ttt	gat	aat	gat	gct	ccg	aag	816	
Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe	Asp	Asn	Asp	Ala	Pro	Lys		

260					265					270						
atc	tac	gaa	gag	gtc	tat	cgt	gtg	gtg	aag	ttc	tgg	gtg	gat	ttg	ggt	864
Ile	Tyr	Glu	Glu	Val	Tyr	Arg	Val	Val	Lys	Phe	Trp	Val	Asp	Leu	Gly	
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gtg	acc	aca	ttc	cgc	gtg	gat	aac	ccg	cac	act	aag	ccc	gct	aat	ttc	912
Val	Thr	Thr	Phe	Arg	Val	Asp	Asn	Pro	His	Thr	Lys	Pro	Ala	Asn	Phe	
		290				295					300					
tgg	cag	tgg	ctt	att	tct	gcc	atc	cat	aaa	tca	aac	cct	gag	gtc	att	960
Trp	Gln	Trp	Leu	Ile	Ser	Ala	Ile	His	Lys	Ser	Asn	Pro	Glu	Val	Ile	
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ttc	cta	gcg	gag	gcg	tct	act	cgc	ccg	gca	cgt	ctg	tat	ttc	ttg	tcc	1008
Phe	Leu	Ala	Glu	Ala	Ser	Thr	Arg	Pro	Ala	Arg	Leu	Tyr	Phe	Leu	Ser	
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aag	att	ggt	ttc	tcc	cag	tct	tac	acc	tac	ttc	acc	tgg	aag	gtc	acc	1056
Lys	Ile	Gly	Phe	Ser	Gln	Ser	Tyr	Thr	Tyr	Phe	Thr	Trp	Lys	Val	Thr	
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Asn	Glu	Glu	Leu	Thr	Glu	Phe	Ala	Thr	Glu	Ile	Ala	Pro	Met	Ala	Asp	
			355				360					365				
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Ile	Ser	Arg	Pro	Asn	Leu	Phe	Val	Asn	Thr	Pro	Asp	Ile	Leu	His	Ala	
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tct	ctg	cag	cat	ggt	gga	cgc	gcc	atg	ttc	gct	atc	cgc	gcc	gca	ttg	1200
Ser	Leu	Gln	His	Gly	Gly	Arg	Ala	Met	Phe	Ala	Ile	Arg	Ala	Ala	Leu	
385					390					395					400	
gcc	gcc	acg	atg	tct	cct	gtg	tgg	ggc	gta	tat	tcc	gga	tat	gag	ctc	1248
Ala	Ala	Thr	Met	Ser	Pro	Val	Trp	Gly	Val	Tyr	Ser	Gly	Tyr	Glu	Leu	
				405					410					415		
ttt	gag	cac	gag	gcc	gtc	aag	cct	ggt	tcg	gaa	gag	tac	ttg	gat	tct	1296
Phe	Glu	His	Glu	Ala	Val	Lys	Pro	Gly	Ser	Glu	Glu	Tyr	Leu	Asp	Ser	
			420					425					430			
gag	aag	tac	gag	ctg	cgt	ccc	cgc	gat	ttc	gag	ggt	gct	ctg	gaa	cgt	1344
Glu	Lys	Tyr	Glu	Leu	Arg	Pro	Arg	Asp	Phe	Glu	Gly	Ala	Leu	Glu	Arg	
			435				440					445				
ggc	gat	tct	ctc	gag	gat	tac	atc	gct	ctg	ctc	aac	cag	atc	cgt	cgc	1392
Gly	Asp	Ser	Leu	Glu	Asp	Tyr	Ile	Ala	Leu	Leu	Asn	Gln	Ile	Arg	Arg	
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gcg	aac	cct	gcc	ttg	cag	caa	cta	cgc	aac	atc	cac	ttc	cac	gaa	gcg	1440
Ala	Asn	Pro	Ala	Leu	Gln	Gln	Leu	Arg	Asn	Ile	His	Phe	His	Glu	Ala	
465					470	</										

gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca 1584
 Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala
 515 520 525

cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca 1632
 Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser
 530 535 540

gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc 1680
 Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile
 545 550 555 560

ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg 1728
 Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp
 565 570 575

cgc gaa atc aag acc tac cgc gcg taatttccca tctctgtacc ttc 1775
 Arg Glu Ile Lys Thr Tyr Arg Ala
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<213> Corynebacterium glutamicum

<400> 360

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 20 25 30

His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu
 35 40 45

Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly
 50 55 60

Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His
 65 70 75 80

Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn
 85 90 95

Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr
 100 105 110

Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro
 115 120 125

Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala
 130 135 140

Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly
 145 150 155 160

Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His
 165 170 175

Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp
 180 185 190
 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu
 195 200 205
 Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu
 210 215 220
 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe
 225 230 235 240
 Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys
 245 250 255
 Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys
 260 265 270
 Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly
 275 280 285
 Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe
 290 295 300
 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile
 305 310 315 320
 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser
 325 330 335
 Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr
 340 345 350
 Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp
 355 360 365
 Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala
 370 375 380
 Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu
 385 390 395 400
 Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu
 405 410 415
 Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser
 420 425 430
 Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg
 435 440 445
 Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg
 450 455 460
 Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala
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 485 490 495
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Cys	Asn	His	His	Asp	Pro	His	Gly	Phe	Tyr	Gly	Trp	His	Glu	Thr	Glu			
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Leu	Leu	Ile	Asp	Asp	Thr	Ser	His	Val	Met	Thr	Pro	Ile	Gly	Asp	Asp			
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Ile	Phe	Ala	Ile	Asp	Leu	Gly	His	Arg	Glu	Arg	Ala	Asp	Tyr	Arg	Leu			
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Tyr	Phe	Leu	Pro	Thr	Val	Gly	Glu	Met	Asp	Ile	Tyr	Leu	Phe	Ser	Glu			

105						110						115						
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Ala	Pro	Asn	Ala	Ile	Gly	Cys	Ala	Val	Val	Gly	Gly	Phe	Asn	Gly	Trp			
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aat	gca	tcc	cag	cat	ccg	atg	cgt	tct	atg	ggt	ggt	tgc	ggt	ctg	tgg	643		
Asn	Ala	Ser	Gln	His	Pro	Met	Arg	Ser	Met	Gly	Gly	Ser	Gly	Leu	Trp			
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gag	ctg	ttc	atc	cca	ggc	ata	gag	gaa	ggc	gaa	gtg	tac	aaa	ttc	gcc	691		
Glu	Leu	Phe	Ile	Pro	Gly	Ile	Glu	Glu	Gly	Glu	Val	Tyr	Lys	Phe	Ala			
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gtc	caa	acc	agg	gaa	ggc	caa	cgt	cgt	gat	aag	gcc	gat	ccg	atg	gct	739		
Val	Gln	Thr	Arg	Glu	Gly	Gln	Arg	Arg	Asp	Lys	Ala	Asp	Pro	Met	Ala			
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cgt	cgc	gca	gaa	ctg	gcg	ccg	gca	acc	gga	tct	att	gtc	gct	tcc	tct	787		
Arg	Arg	Ala	Glu	Leu	Ala	Pro	Ala	Thr	Gly	Ser	Ile	Val	Ala	Ser	Ser			
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Glu	Tyr	Gln	Trp	Gln	Asp	Ser	Glu	Trp	Leu	Arg	Glu	Arg	Ser	Gln	Thr			
230					235					240					245			
gat	ctc	gca	tcc	aag	cca	atg	agt	gtc	tac	gag	gtc	cac	ctc	ggt	tct	883		
Asp	Leu	Ala	Ser	Lys	Pro	Met	Ser	Val	Tyr	Glu	Val	His	Leu	Gly	Ser			
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Trp	Arg	Trp	Gly	Lys	Asn	Tyr	Glu	Asp	Leu	Ala	Thr	Glu	Leu	Val	Asp			
			265					270					275					
tac	gtc	gca	gat	ctt	ggc	tac	acc	cac	gtg	gaa	ttc	ctc	cct	gtc	gca	979		
Tyr	Val	Ala	Asp	Leu	Gly	Tyr	Thr	His	Val	Glu	Phe	Leu	Pro	Val	Ala			
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gag	cac	ccc	ttc	ggt	ggt	tcc	tgg	ggt	tac	cag	gtc	acc	ggc	tac	tac	1027		
Glu	His	Pro	Phe	Gly	Gly	Ser	Trp	Gly	Tyr	Gln	Val	Thr	Gly	Tyr	Tyr			
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gca	ccg	acc	tct	cgt	tgg	ggt	act	cca	gat	cag	ttc	cgt	gcg	cta	gtc	1075		
Ala	Pro	Thr	Ser	Arg	Trp	Gly	Thr	Pro	Asp	Gln	Phe	Arg	Ala	Leu	Val			
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Asp	Ala	Phe	His	Ala	Arg	Gly	Ile	Gly	Val	Ile	Met	Asp	Trp	Val	Pro			
				330					335					340				
gcc	cac	ttc	cct	aag	gat	gat	tgg	gct	ctt	gcc	cgc	ttt	gat	ggc	gaa	1171		
Ala	His	Phe	Pro	Lys	Asp	Asp	Trp	Ala	Leu	Ala	Arg	Phe	Asp	Gly	Glu			
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Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp	
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ggc acc ctg gtc ttt gac ttc ggt cgc aac gaa gtc cgc aac ttc ctc	1267
Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu	
375 380 385	
gtc gct aat gcg ttg tac tgg att gaa gaa ttc cac atc gat ggt ctg	1315
Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe His Ile Asp Gly Leu	
390 395 400 405	
cgc gtc gac gcc gtg gcc tcc atg ctg tac ctc gat tac tcc cgt gag	1363
Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu	
410 415 420	
cac ggc gaa tgg gaa cca aac atc tac ggt ggt cgc gag aac ctc gag	1411
His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly Arg Glu Asn Leu Glu	
425 430 435	
gca gtg cag ttc ctg cag gaa atg aac gcc acg gtg ctg cga ctg cac	1459
Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His	
440 445 450	
cct ggt gcg ctc acc atc gct gag gaa tca act tca tgg cct ggc gtg	1507
Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr Ser Trp Pro Gly Val	
455 460 465	
acc gca cca acg tgg gac ggc ggc ttg gga ttc tcc ctc aag tgg aac	1555
Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn	
470 475 480 485	
atg ggc tgg atg cac gac acc tta gag tac ttc tcc aaa aac cct gtg	1603
Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val	
490 495 500	
cac cgc gca ttc cac cac agt gag ctc act ttc tcc ttg gtg tac gca	1651
His Arg Ala Phe His His Ser Glu Leu Thr Phe Ser Leu Val Tyr Ala	
505 510 515	
ttc tct gag cgt ttt gta ctt ccg atc tct cac gat gaa gtc gtc cac	1699
Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His	
520 525 530	
ggc aag ggt tcc ctg tgg gac cgt atg cct ggc gat acg tgg aac aag	1747
Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys	
535 540 545	
gcc gct ggt ctt cgc acc ttc ctt gcg tac atg tgg tca cac cca ggc	1795
Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly	
550 555 560 565	
aag aag ctg ctt ttc atg ggt cag gag ttt ggt cag cgt gaa gag tgg	1843
Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp	
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gct gaa ggc cag gga ctg cca tgg gat att gtc gac ggc tgg caa ggc	1891
Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly	
585 590 595	

gag tac cac gaa gcc atc cgc act ctg acc cgc tcc ctc aac ggt gtc 1939
 Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val
 600 605 610

tac tca gac tcc cct gcg ctg cac act cag gat ttc acc gga gaa ggc 1987
 Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly
 615 620 625

ttc aca tgg aat aag ggc gac gac gcc acc aac aac att ttg gcg ttc 2035
 Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe
 630 635 640 645

act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg 2083
 Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu
 650 655 660

tct gga acc tcc cag cct gag tac cag ctc ggt gtt gca gcg ggt ggc 2131
 Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly
 665 670 675

gaa tgg aag ctc gtt ctc aac act gat gat gct gaa ttc ctc ggt gca 2179
 Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala
 680 685 690

gaa aac gat atc gct act tcc gtt caa gca gca gcg aca cca cgc gat 2227
 Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala Ala Thr Pro Arg Asp
 695 700 705

aat ttc gcc tac tca ctc tca ctg cat gtc cca gcg atg agt gct cag 2275
 Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro Ala Met Ser Ala Gln
 710 715 720 725

ttc tac tca ctg cag aag taggacacag gaaaatgcat cct 2316
 Phe Tyr Ser Leu Gln Lys
 730

<210> 362

<211> 731

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 362

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Ala Arg Leu Arg His Cys Asn His His Asp Pro His Gly Phe Tyr Gly
 20 25 30

Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly
 35 40 45

Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr
 50 55 60

Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg
 65 70 75 80

Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val
 85 90 95

Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile
 100 105 110
 Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly
 115 120 125
 Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr
 130 135 140
 Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly
 145 150 155 160
 Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly
 165 170 175
 Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu
 180 185 190
 Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys
 195 200 205
 Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser
 210 215 220
 Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg
 225 230 235 240
 Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu
 245 250 255
 Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala
 260 265 270
 Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu
 275 280 285
 Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln
 290 295 300
 Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln
 305 310 315 320
 Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile
 325 330 335
 Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala
 340 345 350
 Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly
 355 360 365
 Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu
 370 375 380
 Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe
 385 390 395 400
 His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu
 405 410 415
 Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly

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Arg	Glu	Asn	Leu	Glu	Ala	Val	Gln	Phe	Leu	Gln	Glu	Met	Asn	Ala	Thr	
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Val	Leu	Arg	Leu	His	Pro	Gly	Ala	Leu	Thr	Ile	Ala	Glu	Glu	Ser	Thr	
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Ser	Trp	Pro	Gly	Val	Thr	Ala	Pro	Thr	Trp	Asp	Gly	Gly	Leu	Gly	Phe	
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Ser	Leu	Lys	Trp	Asn	Met	Gly	Trp	Met	His	Asp	Thr	Leu	Glu	Tyr	Phe	
485					490					495						
Ser	Lys	Asn	Pro	Val	His	Arg	Ala	Phe	His	His	Ser	Glu	Leu	Thr	Phe	
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Ser	Leu	Val	Tyr	Ala	Phe	Ser	Glu	Arg	Phe	Val	Leu	Pro	Ile	Ser	His	
515					520					525						
Asp	Glu	Val	Val	His	Gly	Lys	Gly	Ser	Leu	Trp	Asp	Arg	Met	Pro	Gly	
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Trp	Ser	His	Pro	Gly	Lys	Lys	Leu	Leu	Phe	Met	Gly	Gln	Glu	Phe	Gly	
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Gln	Arg	Glu	Glu	Trp	Ala	Glu	Gly	Gln	Gly	Leu	Pro	Trp	Asp	Ile	Val	
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Ser	Leu	Asn	Gly	Val	Tyr	Ser	Asp	Ser	Pro	Ala	Leu	His	Thr	Gln	Asp	
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Phe	Thr	Gly	Glu	Gly	Phe	Thr	Trp	Asn	Lys	Gly	Asp	Asp	Ala	Thr	Asn	
625					630					635					640	
Asn	Ile	Leu	Ala	Phe	Thr	Arg	Phe	Gly	Ser	Asp	Gly	Ser	Gln	Met	Leu	
645					650					655						
Cys	Val	Phe	Asn	Leu	Ser	Gly	Thr	Ser	Gln	Pro	Glu	Tyr	Gln	Leu	Gly	
660					665					670						
Val	Ala	Ala	Gly	Gly	Glu	Trp	Lys	Leu	Val	Leu	Asn	Thr	Asp	Asp	Ala	
675					680					685						
Glu	Phe	Leu	Gly	Ala	Glu	Asn	Asp	Ile	Ala	Thr	Ser	Val	Gln	Ala	Ala	
690					695					700						
Ala	Thr	Pro	Arg	Asp	Asn	Phe	Ala	Tyr	Ser	Leu	Ser	Leu	His	Val	Pro	
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725					730											

<210> 363

<211> 1913
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1890)
 <223> RXN01884

<400> 363

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cgt ctc cgc gac cta gga atg cgc aac tac tgg ggc tac aac tct ttc 96
Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe
      20             25             30

ggc ttc ttt gcg ccc tac aac gat tac gct gcc aac aag aac ccc ggt 144
Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly
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ggc gcc gtg gcc gag ttc aaa ggc ttg gtg cgc agc tac cac gaa gcg 192
Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala
      50             55             60

ggc ctc gaa gta att ttg gat gtg gtc tac aac cac acc gcc gag ggc 240
Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly
      65             70             75

aac cac atg ggc ccc acc atc gcg ttc cga ggc att gac aac gag gcg 288
Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala
      85             90             95

tac tac cga ctg gtt gag ggc gat cgc cgt cat tac atg gac tac acc 336
Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr
      100            105            110

ggt act ggt aac tcc ctc aat gtc cgc gac ccg cac tca ctg cag ctg 384
Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu
      115            120            125

att atg gat tcg ctg cgc tac tgg gtc acc gag atg cat gtc gac ggc 432
Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly
      130            135            140

ttc cgc ttc gac ctt gcc tct acc ctt gct cgt gaa ttt gat gat gtt 480
Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val
      145            150            155

gac cgc ctg gca acc ttc ttc gac ctg gtc caa caa gac ccg gtg gtc 528
Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val
      165            170            175

tcc cag gtc aag ctc att gct gag ccg tgg gat gtt ggc gaa ggc gga 576
Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly
      180            185            190

tac caa gtg ggt aac ttc cca cca ctg tgg act gag tgg aac ggt aaa 624
Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys
      195            200            205

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Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly Glu Pro Ala Thr Leu	
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ggt gaa ttc gct tcc cga cta act ggt tcc tct gat ttg tat gca aac	720
Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser Asp Leu Tyr Ala Asn	
225 230 235 240	
aac ggc cgt cgc ccc act gca tcg atc aac ttt gtg act gct cac gac	768
Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe Val Thr Ala His Asp	
245 250 255	
ggc ttc acc ctc aat gac ttg gtc agt tac aac gag aag cac aac atg	816
Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn Glu Lys His Asn Met	
260 265 270	
gcc aac ggt gaa gac ggt cgg gac ggt gaa tca cac aac cgt tcc tgg	864
Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser His Asn Arg Ser Trp	
275 280 285	
aac tgt ggc gtc gaa gga cca act gac gat cct gag att atg cag ctg	912
Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro Glu Ile Met Gln Leu	
290 295 300	
cgt gct cag caa cga cgc aac ttc ctc acc acc ttg ttg ctg tcc cag	960
Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr Leu Leu Leu Ser Gln	
305 310 315 320	
ggc acc cct atg ttg tcc cac ggt gat gaa atg gcc cgt acc caa aac	1008
Gly Thr Pro Met Leu Ser His Gly Asp Glu Met Ala Arg Thr Gln Asn	
325 330 335	
ggc aac aac aac gtc tac tgc caa gac aat gaa ctg gcg tgg gtg aat	1056
Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn	
340 345 350	
tgg gat cag gct gaa gaa aac gct gac ttg gtg agc ttc acc agg cgt	1104
Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg	
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Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Gln Phe	
370 375 380	
ctt gcc ggt ggc cct ttg ggc gcc gat gtt cgt gac cgc gat atc gca	1200
Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala	
385 390 395 400	
tgg ctg gta cca aat gga acc ttg atg act caa gat gac tgg gac ttc	1248
Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe	
405 410 415	
gct ttc ggt aaa tca ctg cag gtg ttc ttc aac ggc gat gcc atc gaa	1296
Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu	
420 425 430	
gag cct gat tat cga gga cag aaa atc cac gat gac tcc ttc atc ttg	1344
Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu	
435 440 445	

atg ttc aac gct cac ttc gaa cct atc gat ttc aat ctc cct cct gag 1392
 Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu
 450 455 460

cat ttc ggt atg aag tgg aag ctt ttg gtc gat acc acc gaa gcg gtg 1440
 His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val
 465 470 475 480

ggc cac ccg ctg gag gat ctc acc atc gaa gct ggc gga acc atc act 1488
 Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr
 485 490 495

gtt cct gcc cgt tcc acg atg ctg ctg cgc cag gtg gag gct ccg gac 1536
 Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp
 500 505 510

tac acc aag ctt gag gaa aag atc gct gct gaa aag cgt gag caa gaa 1584
 Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu
 515 520 525

ctt gcg gca gag aag gaa gct gct gag aag cgc gaa ttg gaa ctg gcg 1632
 Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala
 530 535 540

gca gca aag gaa gct gaa gat gct gct gag gct ctc cac ctt gcg gca 1680
 Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Leu His Leu Ala Ala
 545 550 555 560

gaa cgt gct tcg act cag gaa gct gaa ttg gcc cat caa cac ggt gct 1728
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala
 565 570 575

gat gcg att gcc gat gag gta gcg gaa gaa cca caa gag ctg cca caa 1776
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln
 580 585 590

gat gaa gta gcg gca gag gtc gag act gag ccc gac acc gag cct gac 1824
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp
 595 600 605

act gaa tct gac tcc gag cag gct gag gta gct tca gag gag cct gaa 1872
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu
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<210> 364

<211> 630

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp
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Gly	Ala	Val	Ala	Glu	Phe	Lys	Gly	Leu	Val	Arg	Ser	Tyr	His	Glu	Ala
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Gly	Leu	Glu	Val	Ile	Leu	Asp	Val	Val	Tyr	Asn	His	Thr	Ala	Glu	Gly
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Asn	His	Met	Gly	Pro	Thr	Ile	Ala	Phe	Arg	Gly	Ile	Asp	Asn	Glu	Ala
				85					90					95	
Tyr	Tyr	Arg	Leu	Val	Glu	Gly	Asp	Arg	Arg	His	Tyr	Met	Asp	Tyr	Thr
			100					105					110		
Gly	Thr	Gly	Asn	Ser	Leu	Asn	Val	Arg	Asp	Pro	His	Ser	Leu	Gln	Leu
		115					120					125			
Ile	Met	Asp	Ser	Leu	Arg	Tyr	Trp	Val	Thr	Glu	Met	His	Val	Asp	Gly
	130					135					140				
Phe	Arg	Phe	Asp	Leu	Ala	Ser	Thr	Leu	Ala	Arg	Glu	Phe	Asp	Asp	Val
	145				150					155					160
Asp	Arg	Leu	Ala	Thr	Phe	Phe	Asp	Leu	Val	Gln	Gln	Asp	Pro	Val	Val
				165					170					175	
Ser	Gln	Val	Lys	Leu	Ile	Ala	Glu	Pro	Trp	Asp	Val	Gly	Glu	Gly	Gly
			180					185					190		
Tyr	Gln	Val	Gly	Asn	Phe	Pro	Pro	Leu	Trp	Thr	Glu	Trp	Asn	Gly	Lys
		195					200					205			
Tyr	Arg	Asp	Thr	Val	Arg	Asp	Phe	Trp	Arg	Gly	Glu	Pro	Ala	Thr	Leu
	210					215					220				
Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser	Asp	Leu	Tyr	Ala	Asn
	225				230					235					240
Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	Val	Thr	Ala	His	Asp
				245				250						255	
Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	Glu	Lys	His	Asn	Met
			260					265					270		
Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	His	Asn	Arg	Ser	Trp
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Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro	Glu	Ile	Met	Gln	Leu
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Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr	Leu	Leu	Leu	Ser	Gln
	305				310					315					320
Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	Ala	Arg	Thr	Gln	Asn
				325					330					335	
Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	Leu	Ala	Trp	Val	Asn
			340					345					350		
Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	Ser	Phe	Thr	Arg	Arg

355					360					365					
Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe	Arg	Arg	Arg	Gln	Phe
370						375					380				
Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg	Asp	Arg	Asp	Ile	Ala
385					390					395					400
Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	Asp	Asp	Trp	Asp	Phe
				405					410					415	
Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn	Gly	Asp	Ala	Ile	Glu
			420					425					430		
Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp	Asp	Ser	Phe	Ile	Leu
		435					440					445			
Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe	Asn	Leu	Pro	Pro	Glu
	450					455					460				
His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp	Thr	Thr	Glu	Ala	Val
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Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala	Gly	Gly	Thr	Ile	Thr
				485					490					495	
Val	Pro	Ala	Arg	Ser	Thr	Met	Leu	Leu	Arg	Gln	Val	Glu	Ala	Pro	Asp
			500				505						510		
Tyr	Thr	Lys	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Glu	Lys	Arg	Glu	Gln	Glu
		515					520					525			
Leu	Ala	Ala	Glu	Lys	Glu	Ala	Ala	Glu	Lys	Arg	Glu	Leu	Glu	Leu	Ala
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Ala	Ala	Lys	Glu	Ala	Glu	Asp	Ala	Ala	Glu	Ala	Leu	His	Leu	Ala	Ala
545					550					555					560
Glu	Arg	Ala	Ser	Thr	Gln	Glu	Ala	Glu	Leu	Ala	His	Gln	His	Gly	Ala
				565					570					575	
Asp	Ala	Ile	Ala	Asp	Glu	Val	Ala	Glu	Glu	Pro	Gln	Glu	Leu	Pro	Gln
			580					585					590		
Asp	Glu	Val	Ala	Ala	Glu	Val	Glu	Thr	Glu	Pro	Asp	Thr	Glu	Pro	Asp
		595					600					605			
Thr	Glu	Ser	Asp	Ser	Glu	Gln	Ala	Glu	Val	Ala	Ser	Glu	Glu	Pro	Glu
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<210> 365

<211> 1496

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1473)

<223> FRXA01884

<400> 365

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gaa ttt gat gat gtt gac cgc ctg gca acc ttc ttc gac ctg gtc caa	96
Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln	
20 25 30	
caa gac ccg gtg gtc tcc cag gtc aag ctc att gct gag ccg tgg gat	144
Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp	
35 40 45	
gtt ggc gaa ggc gga tac caa gtg ggt aac ttc cca cca ctg tgg act	192
Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr	
50 55 60	
gag tgg aac ggt aaa tac cgc gac act gtc cgt gat ttc tgg cgt ggt	240
Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly	
65 70 75 80	
gag cca gca acc ttg ggt gaa ttc gct tcc cga cta act ggt tcc tct	288
Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser	
85 90 95	
gat ttg tat gca aac aac ggc cgt cgc ccc act gca tcg atc aac ttt	336
Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe	
100 105 110	
gtg act gct cac gac ggc ttc acc ctc aat gac ttg gtc agt tac aac	384
Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn	
115 120 125	
gag aag cac aac atg gcc aac ggt gaa gac ggt cgg gac ggt gaa tca	432
Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser	
130 135 140	
cac aac cgt tcc tgg aac tgt ggc gtc gaa gga cca act gac gat cct	480
His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro	
145 150 155 160	
gag att atg cag ctg cgt gct cag caa cga cgc aac ttc ctc acc acc	528
Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr	
165 170 175	
ttg ttg ctg tcc cag ggc acc cct atg ttg tcc cac ggt gat gaa atg	576
Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met	
180 185 190	
gcc cgt acc caa aac ggc aac aac aac gtc tac tgc caa gac aat gaa	624
Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu	
195 200 205	
ctg gcg tgg gtg aat tgg gat cag gct gaa gaa aac gct gac ttg gtg	672
Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val	
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Arg	Arg	Arg	Gln	Phe	Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg	
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gac	cgc	gat	atc	gca	tgg	ctg	gta	cca	aat	gga	acc	ttg	atg	act	caa	816
Asp	Arg	Asp	Ile	Ala	Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	
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Asp	Asp	Trp	Asp	Phe	Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn	
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aat	ctc	cct	cct	gag	cat	ttc	ggt	atg	aag	tgg	aag	ctt	ttg	gtc	gat	1008
Asn	Leu	Pro	Pro	Glu	His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp	
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acc	acc	gaa	gcg	gtg	ggc	cac	ccg	ctg	gag	gat	ctc	acc	atc	gaa	gct	1056
Thr	Thr	Glu	Ala	Val	Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala	
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Gly	Gly	Thr	Ile	Thr	Val	Pro	Ala	Arg	Ser	Thr	Met	Leu	Leu	Arg	Gln	
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gtg	gag	gct	ccg	gac	tac	acc	aag	ctt	gag	gaa	aag	atc	gct	gct	gaa	1152
Val	Glu	Ala	Pro	Asp	Tyr	Thr	Lys	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Glu	
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Lys	Arg	Glu	Gln	Glu	Leu	Ala	Ala	Glu	Lys	Glu	Ala	Ala	Glu	Lys	Arg	
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Glu	Leu	Glu	Leu	Ala	Ala	Ala	Lys	Glu	Ala	Glu	Asp	Ala	Ala	Glu	Ala	
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ctc	cac	ctt	gcg	gca	gaa	cgt	gct	tcg	act	cag	gaa	gct	gaa	ttg	gcc	1296
Leu	His	Leu	Ala	Ala	Glu	Arg	Ala	Ser	Thr	Gln	Glu	Ala	Glu	Leu	Ala	
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His	Gln	His	Gly	Ala	Asp	Ala	Ile	Ala	Asp	Glu	Val	Ala	Glu	Glu	Pro	
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Gln	Glu	Leu	Pro	Gln	Asp	Glu	Val	Ala	Ala	Glu	Val	Glu	Thr	Glu	Pro	
	450					455					460					
gac	acc	gag	cct	gac	act	gaa	tct	gac	tcc	gag	cag	gct	gag	gta	gct	1440
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Gly	Asp	Ala	Ile	Glu	Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp				
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Thr	Thr	Glu	Ala	Val	Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala				
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Val	Glu	Ala	Pro	Asp	Tyr	Thr	Lys	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Glu				
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Lys	Arg	Glu	Gln	Glu	Leu	Ala	Ala	Glu	Lys	Glu	Ala	Ala	Glu	Lys	Arg				
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Leu	His	Leu	Ala	Ala	Glu	Arg	Ala	Ser	Thr	Gln	Glu	Ala	Glu	Leu	Ala				
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His	Gln	His	Gly	Ala	Asp	Ala	Ile	Ala	Asp	Glu	Val	Ala	Glu	Glu	Pro				
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Gln	Glu	Leu	Pro	Gln	Asp	Glu	Val	Ala	Ala	Glu	Val	Glu	Thr	Glu	Pro				
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Asp	Thr	Glu	Pro	Asp	Thr	Glu	Ser	Asp	Ser	Glu	Gln	Ala	Glu	Val	Ala				
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<213> Corynebacterium glutamicum

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<221> CDS

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act	cac	cca	gtg	ttg	gct	atc	cct	gag	ctt	atg	cgt	ctg	ctc	atg	gac	163
Thr	His	Pro	Val	Leu	Ala	Ile	Pro	Glu	Leu	Met	Arg	Leu	Leu	Met	Asp	
				10					15					20		
gag	cat	gac	atg	ggc	tgg	gaa	gaa	tcc	tgg	gca	atc	gtg	ttc	aag	acc	211
Glu	His	Asp	Met	Gly	Trp	Glu	Glu	Ser	Trp	Ala	Ile	Val	Phe	Lys	Thr	
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Phe	Ala	Tyr	Thr	Asn	His	Thr	Val	Leu	Thr	Glu	Ala	Leu	Glu	Gln	Trp	
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Asp	Gln	Gln	Ile	Phe	Gln	Gln	Leu	Phe	Trp	Arg	Val	Trp	Glu	Ile	Ile	
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Thr	Glu	Ile	Asp	Arg	Arg	Phe	Arg	Leu	Glu	Arg	Ala	Ala	Asp	Gly	Leu	
	70				75					80					85	
gat	gaa	gag	acc	atc	gac	cgc	atg	gct	cca	atc	cag	cac	ggc	act	gtt	403
Asp	Glu	Glu	Thr	Ile	Asp	Arg	Met	Ala	Pro	Ile	Gln	His	Gly	Thr	Val	
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Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr	
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cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc	595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu	
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Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu	
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Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu	
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cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc	739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu	
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gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag	787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln	
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Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr	
230 235 240 245	
gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc	883
Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile	
250 255 260	
cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc	931
Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val	
265 270 275	
cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta	979
Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val	
280 285 290	
aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag	1027
Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu	
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aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc	1075
Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val	
310 315 320 325	
tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac	1123
Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn	
330 335 340	
atg aag ttc atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc	1171
Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly	
345 350 355	

gcc aac gta gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc 1219
 Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile
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 Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu
 375 380 385

cca tat gag ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac 1315
 Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp
 390 395 400 405

gcc ctg gat aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac 1363
 Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr
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gac ctc aag cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac 1411
 Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp
 425 430 435

acc tac tac gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac 1459
 Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp
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cgt atg gcc gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg 1507
 Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met
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gcc tgg atc aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc 1555
 Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr
 470 475 480 485

atc cgc gat tat gcc acc gag atc tgg aag ctc gag cca act cct gct 1603
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<213> Corynebacterium glutamicum

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 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg
 50 55 60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg
 65 70 75 80

Ala Ala Asp Gly Leu Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile
 85 90 95
 Gln His Gly Thr Val His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr
 100 105 110
 Ser Ile Asn Gly Val Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu
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 Thr Leu Ala Asp Trp Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys
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 Thr Asn Gly Val Thr Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly
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 Leu Ser Asp Leu Leu Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr
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 Asp Leu Asp Glu Leu Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser
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 Val Leu Glu Glu Leu Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe
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 Ala Glu Trp Ile Leu Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser
 210 215 220
 Ile Phe Asp Val Gln Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu
 225 230 235 240
 Met Asn Ala Leu Tyr Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp
 245 250 255
 Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala
 260 265 270
 Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser
 275 280 285
 Ile Ala Asp Leu Val Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys
 290 295 300
 Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu
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 Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala
 325 330 335
 Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu
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 Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu
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gat	cgc	cgc	ttc	cgt	ttg	gag	cgc	gca	gcc	gat	gga	ctg	gat	gaa	gag	96	
Asp	Arg	Arg	Phe	Arg	Leu	Glu	Arg	Ala	Ala	Asp	Gly	Leu	Asp	Glu	Glu		
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Thr	Ile	Asp	Arg	Met	Ala	Pro	Ile	Gln	Arg	Gly	Thr	Val	His	Met	Ala		
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tgg	att	gcc	tgt	tac	gcg	gca	tat	tcc	atc	aat	ggc	gtg	gca	gcg	ctg	192	
Trp	Ile	Ala	Cys	Tyr	Ala	Ala	Tyr	Ser	Ile	Asn	Gly	Val	Ala	Ala	Leu		
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cac	acc	gag	atc	atc	aag	gcc	gag	acc	ttg	gct	gac	tgg	tac	gca	ctg	240	
His	Thr	Glu	Ile	Ile	Lys	Ala	Glu	Thr	Leu	Ala	Asp	Trp	Tyr	Ala	Leu		
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Trp	Pro	Glu	Lys	Phe	Asn	Asn	Lys	Thr	Asn	Gly	Val	Thr	Pro	Arg	Arg		
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tgg	ctg	cgc	atg	atc	aac	cca	ggt	ctg	tct	gac	ctg	ctc	act	cga	ctt	336	
Trp	Leu	Arg	Met	Ile	Asn	Pro	Gly	Leu	Ser	Asp	Leu	Leu	Thr	Arg	Leu		
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Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu	
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Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile	
130 135 140	
aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc gag cgc cag	480
Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln	
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Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg	
165 170 175	
ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac gta cta gac	576
Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp	
180 185 190	
ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc cca gca cgc	624
Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg	
195 200 205	
act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc cgc gcc aag	672
Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys	
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Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp	
225 230 235 240	
cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag aac tac aac	768
Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn	
245 250 255	
gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc tcc gaa cag	816
Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln	
260 265 270	
att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac atg aag ttc	864
Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe	
275 280 285	
atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc gcc aac gta	912
Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val	
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gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc ttc ggt gct	960
Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala	
305 310 315 320	
cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag cca tat gag	1008
Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu	
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ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac gcc ctg gat	1056
Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp	
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Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
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Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
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Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu
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Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile
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Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln
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 Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg
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 Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys
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 Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp
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 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn
 245 250 255
 Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln
 260 265 270
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 275 280 285
 Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val
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 Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu
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 Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp
 340 345 350
 Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
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 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
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 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
 385 390 395 400
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
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 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
 420 425 430
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
 435 440 445

<210> 373

<211> 2348

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(2325)

<223> RXN02100

<400> 373

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Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser	
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gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga	96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly	
20 25 30	
gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc	144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser	
35 40 45	
ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg	192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met	
50 55 60	
aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc	240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu	
65 70 75 80	
tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	

aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg 210 215 220	672
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala 225 230 235 240	720
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg 245 250 255	768
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu 260 265 270	816
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 275 280 285	864
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu 290 295 300	912
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 305 310 315 320	960
agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu 325 330 335	1008
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val 340 345 350	1056
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp 355 360 365	1104
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu 370 375 380	1152
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val 385 390 395 400	1200
gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu 405 410 415	1248
gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr 420 425 430	1296
att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met 435 440 445	1344
ctg cgc aac cct gaa cgc ctg cgt tcc atc ttg ctt aat gag gaa cgc	1392

Leu	Arg	Asn	Pro	Glu	Arg	Leu	Arg	Ser	Ile	Leu	Leu	Asn	Glu	Glu	Arg		
450						455				460							
cca	gtt	cag	ttc	gtt	att	gct	ggg	aag	gca	cac	cca	cat	gac	atg	ggg	1440	
Pro	Val	Gln	Phe	Val	Ile	Ala	Gly	Lys	Ala	His	Pro	His	Asp	Met	Gly		
465					470				475						480		
ggc	aag	aag	ctc	atg	cag	gaa	atc	gtc	cac	ttc	gct	gat	caa	gct	ggg	1488	
Gly	Lys	Lys	Leu	Met	Gln	Glu	Ile	Val	His	Phe	Ala	Asp	Gln	Ala	Gly		
				485					490					495			
gtc	cgt	gac	cgt	ttc	ctc	ttc	ctg	cct	gat	tac	gac	atc	aac	ctg	gcc	1536	
Val	Arg	Asp	Arg	Phe	Leu	Phe	Leu	Pro	Asp	Tyr	Asp	Ile	Asn	Leu	Ala		
			500					505					510				
agc	tac	ctg	atc	tct	ggg	gct	gac	gtg	tgg	ctg	aac	aac	cca	gtg	cgc	1584	
Ser	Tyr	Leu	Ile	Ser	Gly	Ala	Asp	Val	Trp	Leu	Asn	Asn	Pro	Val	Arg		
		515					520					525					
cct	cag	gaa	gca	tcg	gga	acc	tcc	ggg	atg	aag	gcc	gtc	atg	aat	ggg	1632	
Pro	Gln	Glu	Ala	Ser	Gly	Thr	Ser	Gly	Met	Lys	Ala	Val	Met	Asn	Gly		
		530				535					540						
ggc	ctg	acc	ctg	tcc	atc	tct	gat	ggg	tgg	tgg	gat	gaa	atg	cct	aag	1680	
Gly	Leu	Thr	Leu	Ser	Ile	Ser	Asp	Gly	Trp	Trp	Asp	Glu	Met	Pro	Lys		
545					550				555						560		
gag	acc	acc	ggc	tgg	acc	atc	cca	acc	gtt	gag	tcc	cag	gac	ttg	gaa	1728	
Glu	Thr	Thr	Gly	Trp	Thr	Ile	Pro	Thr	Val	Glu	Ser	Gln	Asp	Leu	Glu		
			565					570						575			
tgc	cgc	gac	cac	ctg	gaa	tcc	cag	gcg	ctg	tac	gac	ctg	ctg	gaa	aac	1776	
Cys	Arg	Asp	His	Leu	Glu	Ser	Gln	Ala	Leu	Tyr	Asp	Leu	Leu	Glu	Asn		
			580					585					590				
gaa	gtt	gca	ccg	ctg	ttt	tac	aag	cgc	gac	aag	aac	ggc	atc	cca	cag	1824	
Glu	Val	Ala	Pro	Leu	Phe	Tyr	Lys	Arg	Asp	Lys	Asn	Gly	Ile	Pro	Gln		
		595					600					605					
gac	tgg	ctg	gac	ctg	gtt	cgc	gaa	tcc	tgg	acc	acc	ctg	tca	cca	atg	1872	
Asp	Trp	Leu	Asp	Leu	Val	Arg	Glu	Ser	Trp	Thr	Thr	Leu	Ser	Pro	Met		
	610					615						620					
gtc	acc	tcc	acc	cgc	atg	gtg	cgc	gac	tac	acc	acc	cag	tac	tac	cgc	1920	
Val	Thr	Ser	Thr	Arg	Met	Val	Arg	Asp	Tyr	Thr	Thr	Gln	Tyr	Tyr	Arg		
625					630				635						640		
cca	acc	aaa	cac	cag	gca	gag	ctc	att	gcg	cag	cct	gca	gaa	gca	gcg	1968	
Pro	Thr	Lys	His	Gln	Ala	Glu	Leu	Ile	Ala	Gln	Pro	Ala	Glu	Ala	Ala		
			645						650					655			
gat	tac	gcg	gca	tgg	ctt	gag	cac	atc	aaa	gca	gag	tgg	gct	ggc	gtc	2016	
Asp	Tyr	Ala	Ala	Trp	Leu	Glu	His	Ile	Lys	Ala	Glu	Trp	Ala	Gly	Val		
			660					665					670				
aag	gtc	tca	gac	ctg	aag	atc	agc	gag	agc	gcc	atc	acg	gcg	cag	gag	2064	
Lys	Val	Ser	Asp	Leu	Lys	Ile	Ser	Glu	Ser	Ala	Ile	Thr	Ala	Gln	Glu		
		675					680					685					
ctt	gaa	gtc	agc	gtt	cgc	gtt	gat	tcc	ggg	tcg	ctt	aac	gac	gac	gag	2112	
Leu	Glu	Val	Ser	Val	Arg	Val	Asp	Ser	Gly	Ser	Leu	Asn	Asp	Asp	Glu		

690	695	700	
ttc caa gct cag gca ctc ttt ggt gcg ctc gga cac aac ggt gac atc			2160
Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile			
705	710	715	720
gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac			2208
Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr			
725	730		735
gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc			2256
Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala			
740	745		750
cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc			2304
Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg			
755	760		765
ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa			2348
Leu Ile Thr Tyr Leu Glu Asn			
770	775		

<210> 374

<211> 775

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

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20 25 30

Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
35 40 45

Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
50 55 60

Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
65 70 75 80

Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
85 90 95

Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
100 105 110

Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
115 120 125

Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
130 135 140

Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
145 150 155 160

Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
165 170 175

Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400
 Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu
 405 410 415
 Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr
 420 425 430
 Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met
 435 440 445
 Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg
 450 455 460
 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly
 465 470 475 480
 Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly
 485 490 495

Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala
 500 505 510
 Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg
 515 520 525
 Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly
 530 535 540
 Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys
 545 550 555 560
 Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu
 565 570 575
 Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn
 580 585 590
 Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln
 595 600 605
 Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met
 610 615 620
 Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg
 625 630 635 640
 Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala
 645 650 655
 Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val
 660 665 670
 Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu
 675 680 685
 Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu
 690 695 700
 Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile
 705 710 715 720
 Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr
 725 730 735
 Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala
 740 745 750
 Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg
 755 760 765
 Leu Ile Thr Tyr Leu Glu Asn
 770 775

<210> 375

<211> 941

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(918)

<223> FRXA02100

<400> 375

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Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met	
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cag gaa atc gtc cac ttc gct gat caa gct ggt gtc cgt gac cgt ttc	96
Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe	
20 25 30	
ctc ttc ctg cct gat tac gac atc aac ctg gcc agc tac ctg atc tct	144
Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser	
35 40 45	
ggt gct gac gtg tgg ctg aac aac cca gtg cgc cct cag gaa gca tgc	192
Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser	
50 55 60	
gga acc tcc ggt atg aag gcc gtc atg aat ggt ggc ctg acc ctg tcc	240
Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser	
65 70 75 80	
atc tct gat ggt tgg tgg gat gaa atg cct aag gag acc acc ggc tgg	288
Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp	
85 90 95	
acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg	336
Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu	
100 105 110	
gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg	384
Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu	
115 120 125	
ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg	432
Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu	
130 135 140	
gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc	480
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg	
145 150 155 160	
atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag	528
Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln	
165 170 175	
gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg	576
Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp	
180 185 190	
ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg	624
Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu	
195 200 205	
aag atc agc gag agc gcc atc acg gcg cag gag ctt gaa gtc agc gtt	672
Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val	
210 215 220	

cgc gtt gat tcc ggt tcg ctt aac gac gac gag ttc caa gct cag gca 720
 Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240

ctc ttt ggt gcg ctc gga cac aac ggt gac atc gaa gat cca gaa atc 768
 Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255

acc gtt ttg acc cca cgc ggc gat ggc gcc tac gcg gca aag gtc agc 816
 Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270

act gac ctg cca ggc aac tac ggc atc act gcc cgc gtt gtt cca aac 864
 Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285

aac agg atg ctg gtc agc cca gcg gaa acc cgc ctg atc acc tac ttg 912
 Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
 290 295 300

gag aac tagggcgaaa ctagctttac caa 941
 Glu Asn
 305

<210> 376

<211> 306

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met
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 20 25 30

Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser
 35 40 45

Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser
 50 55 60

Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser
 65 70 75 80

Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp
 85 90 95

Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
 100 105 110

Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
 115 120 125

Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
 130 135 140

Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
 145 150 155 160

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
 165 170 175

Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
 180 185 190

Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
 195 200 205

Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
 210 215 220

Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240

Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255

Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270

Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285

Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
 290 295 300

Glu Asn
 305

<210> 377
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1206)
 <223> FRXA02113

<400> 377

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gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga	96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly	
20 25 30	
gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc	144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser	
35 40 45	
ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg	192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met	
50 55 60	
aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc	240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu	
65 70 75 80	

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
ggt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc	768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
245 250 255	
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa	816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	

agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa 1008
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc 1056
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat 1104
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag 1152
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt 1200
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
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 Ala Arg

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 <213> Corynebacterium glutamicum

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 35 40 45
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
 50 55 60
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65 70 75 80
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
 85 90 95
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
 100 105 110
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
 115 120 125
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
 130 135 140
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
 145 150 155 160

Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
 165 170 175
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
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 Ala Arg

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 <223> RXA02147

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Met Phe Gly Arg Arg	
1 5	
tgg gtg agc gtt gtg gcg tca tgt gtt atc gca agc acg ctg att ctg	163
Trp Val Ser Val Val Ala Ser Cys Val Ile Ala Ser Thr Leu Ile Leu	
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gtg cct tcg cat tcc ggt gcg gag gaa gtc gat caa ctg att gct gat	211
Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp	
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atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa	259
Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys	
40 45 50	
cag ctt gag att gat att gag gct cgt gag gtc acg atc aag gaa gtt	307
Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Ile Lys Glu Val	
55 60 65	
cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag	355
Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu	
70 75 80 85	
aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag	403
Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys	
90 95 100	
tat cgt ggc aca gtc acg gat cct ttg agc att gcg gtg tct gca gaa	451
Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile Ala Val Ser Ala Glu	
105 110 115	
gat cca caa aac gtg att gat cgg atg agc tac ctt tca acg ttg act	499
Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr Leu Ser Thr Leu Thr	
120 125 130	
aag tcc act agt gat gtg gtt gaa tcc ctc aac gcg gag act gag aag	547
Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn Ala Glu Thr Glu Lys	
135 140 145	
tcc gca gaa gct gtg tat caa gca aac cgt act aag gcg gaa gcg gag	595
Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr Lys Ala Glu Ala Glu	
150 155 160 165	
ttc cag ttg ggg cag ctg aag gta cgc cag gcg gag ctt gaa tct gaa	643
Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala Glu Leu Glu Ser Glu	
170 175 180	
aag gaa gca ttg gat ggt cga aaa tcg gag atc cga gac cgg gtg gat	691
Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile Arg Asp Arg Val Asp	
185 190 195	
gcc ctg acg cca cag gag cgg gaa atg tgg gtt gct aag aat ggt cca	739
Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val Ala Lys Asn Gly Pro	
200 205 210	
ttg gac att gat ctg act gat ttg ctt ggt ctt tcc gct gcg act tcg	787
Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu Ser Ala Ala Thr Ser	
215 220 225	

ggt gcg gtg gat gct gcc ttg tct aag ttg gga agc cct tat ggt tgg 835
 Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly Ser Pro Tyr Gly Trp
 230 235 240 245
 ggt ggc att ggc cca aat gag ttt gat tgc tca ggt ttg atc tat tgg 883
 Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser Gly Leu Ile Tyr Trp
 250 255 260
 gcg tat cag cag atg ggt aag act ttg cca cgt acg tct caa gct cag 931
 Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg Thr Ser Gln Ala Gln
 265 270 275
 atg gct ggc gga acg ccg gtg agc aga gat gag ctg cag cct ggc gat 979
 Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu Leu Gln Pro Gly Asp
 280 285 290
 gtc att gga tat tac cca ggt gct act cac gtg gga ctg tat att ggg 1027
 Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val Gly Leu Tyr Ile Gly
 295 300 305
 gac gga aag att gtg cac gcc tca gac tac gga atc cct gtg cag gtg 1075
 Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly Ile Pro Val Gln Val
 310 315 320 325
 gta tct gtt gat tca gca ccg ttt tat ggt gcg cgt cgc tac 1117
 Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala Arg Arg Tyr
 330 335
 taagaaatag ttcgtcagga gaa 1140

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<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

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 Gln Leu Ile Ala Asp Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln
 35 40 45
 Asn Glu Glu Val Lys Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val
 50 55 60
 Thr Ile Lys Glu Val Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala
 65 70 75 80
 Asp Gln Ala Ser Glu Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg
 85 90 95
 Ile Ala Gln Ala Lys Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile
 100 105 110
 Ala Val Ser Ala Glu Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr
 115 120 125

Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn
 130 135 140
 Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr
 145 150 155 160
 Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala
 165 170 175
 Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile
 180 185 190
 Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val
 195 200 205
 Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu
 210 215 220
 Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly
 225 230 235 240
 Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser
 245 250 255
 Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg
 260 265 270
 Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu
 275 280 285
 Leu Gln Pro Gly Asp Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val
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 Gly Leu Tyr Ile Gly Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly
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 Ile Pro Val Gln Val Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala
 325 330 335

Arg Arg Tyr

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 <223> RXA01478

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tattggagtc acctggcctg aaatcctcta ctctgggcgc atg acc att cca gga 115
 Met Thr Ile Pro Gly
 1 5

gct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac 163

Ala	Ser	Thr	Gln	Thr	Asp	Ile	Pro	Leu	Asp	Thr	Leu	Leu	Glu	Asp	Tyr	
				10					15					20		
gcg	cta	ctg	tca	gac	act	cac	acc	ggc	gct	ctg	ctg	tcc	aac	atg	ggc	211
Ala	Leu	Leu	Ser	Asp	Thr	His	Thr	Gly	Ala	Leu	Leu	Ser	Asn	Met	Gly	
			25					30					35			
agt	ttg	gac	tgg	ttg	tgc	ctg	cct	cgt	ttt	gat	tcc	caa	gcc	atg	ttc	259
Ser	Leu	Asp	Trp	Leu	Cys	Leu	Pro	Arg	Phe	Asp	Ser	Gln	Ala	Met	Phe	
		40					45					50				
acc	agg	ctg	ctt	ggg	gat	cgc	gag	cac	gga	cac	tgg	agt	ttg	cgt	gtc	307
Thr	Arg	Leu	Leu	Gly	Asp	Arg	Glu	His	Gly	His	Trp	Ser	Leu	Arg	Val	
	55					60					65					
cca	ggg	ggg	gag	gtg	atc	agc	caa	aac	tac	ctc	ggc	gat	tcc	ttc	gtg	355
Pro	Gly	Gly	Glu	Val	Ile	Ser	Gln	Asn	Tyr	Leu	Gly	Asp	Ser	Phe	Val	
	70				75					80					85	
gtg	cag	acc	gtg	tgg	cgt	tca	gag	acc	ggg	act	gcc	cgg	gtt	gtt	gat	403
Val	Gln	Thr	Val	Trp	Arg	Ser	Glu	Thr	Gly	Thr	Ala	Arg	Val	Val	Asp	
				90					95					100		
ttc	atg	cca	att	cac	ggg	caa	gaa	caa	ccc	gat	atc	acc	gac	ctg	gtg	451
Phe	Met	Pro	Ile	His	Gly	Gln	Glu	Gln	Pro	Asp	Ile	Thr	Asp	Leu	Val	
			105					110					115			
cgc	tct	gtg	cac	tgc	gtg	gaa	ggc	gaa	gtg	gat	gtg	gaa	tcg	atc	ctg	499
Arg	Ser	Val	His	Cys	Val	Glu	Gly	Glu	Val	Asp	Val	Glu	Ser	Ile	Leu	
		120					125					130				
cgc	ctg	cgt	ttt	gat	tat	ggc	gag	tcc	act	ccg	tat	ttc	cgc	acc	agc	547
Arg	Leu	Arg	Phe	Asp	Tyr	Gly	Glu	Ser	Thr	Pro	Tyr	Phe	Arg	Thr	Ser	
	135					140					145					
act	gtc	gac	ggc	atc	agc	atc	gtg	cag	gct	gtc	gcc	ggc	ccc	aat	gcg	595
Thr	Val	Asp	Gly	Ile	Ser	Ile	Val	Gln	Ala	Val	Ala	Gly	Pro	Asn	Ala	
	150				155					160					165	
gta	tat	gtt	cgt	gga	cct	gag	atg	cca	cac	cgc	cct	gca	aag	gat	tgt	643
Val	Tyr	Val	Arg	Gly	Pro	Glu	Met	Pro	His	Arg	Pro	Ala	Lys	Asp	Cys	
				170					175					180		
cac	agt	ggc	acc	ttc	cac	ctg	acg	gcc	ggc	gaa	tcc	gtg	gaa	tgg	gtt	691
His	Ser	Gly	Thr	Phe	His	Leu	Thr	Ala	Gly	Glu	Ser	Val	Glu	Trp	Val	
			185					190					195			
ctc	acc	tgg	gca	ccg	tcg	ttc	gaa	ccg	cat	ccc	ccc	atg	ccg	gat	tac	739
Leu	Thr	Trp	Ala	Pro	Ser	Phe	Glu	Pro	His	Pro	Pro	Met	Pro	Asp	Tyr	
		200					205					210				
acc	cgc	tct	ttg	gag	agc	acc	ttg	agc	ttc	tgg	gca	tca	tgg	gtt	gaa	787
Thr	Arg	Ser	Leu	Glu	Ser	Thr	Leu	Ser	Phe	Trp	Ala	Ser	Trp	Val	Glu	
	215					220					225					
gag	ctc	ccc	cac	cag	cgc	ctc	tac	gac	gct	gaa	gtc	cgc	cgc	tcc	atg	835
Glu	Leu	Pro	His	Gln	Arg	Leu	Tyr	Asp	Ala	Glu	Val	Arg	Arg	Ser	Met	
	230				235					240					245	
ctc	gta	ctg	cgc	gcc	ttg	acc	gat	cta	caa	acc	ggg	ggc	atc	gtg	gcc	883
Leu	Val	Leu	Arg	Ala	Leu	Thr	Asp	Leu	Gln	Thr	Gly	Gly	Ile	Val	Ala	

250										255										260									
gca	ccg	acc	acc	tca	cta	cca	gag	gat	ttc	gga	ggc	atc	cgt	aac	tgg					931									
Ala	Pro	Thr	Thr	Ser	Leu	Pro	Glu	Asp	Phe	Gly	Gly	Ile	Arg	Asn	Trp														
			265					270					275																
gac	tac	cgc	tac	gtg	tgg	ctg	cgc	gac	tcc	gca	ctc	acc	att	gaa	gcc					979									
Asp	Tyr	Arg	Tyr	Val	Trp	Leu	Arg	Asp	Ser	Ala	Leu	Thr	Ile	Glu	Ala														
		280					285					290																	
ctc	gtg	gaa	tac	gga	ttc	tcc	caa	gca	gcc	ctc	caa	tgg	cgc	acc	tgg					1027									
Leu	Val	Glu	Tyr	Gly	Phe	Ser	Gln	Ala	Ala	Leu	Gln	Trp	Arg	Thr	Trp														
		295				300					305																		
ctg	ctg	cgc	gcc	atc	gca	ggc	gac	ccg	gaa	aac	ctc	cgc	atc	atg	tat					1075									
Leu	Leu	Arg	Ala	Ile	Ala	Gly	Asp	Pro	Glu	Asn	Leu	Arg	Ile	Met	Tyr														
310					315					320					325														
ggc	ctc	ggc	ggc	gaa	cga	cac	ctc	cct	gaa	cgc	gaa	ctc	caa	cac	ctg					1123									
Gly	Leu	Gly	Gly	Glu	Arg	His	Leu	Pro	Glu	Arg	Glu	Leu	Gln	His	Leu														
				330				335						340															
cgc	gga	tac	gaa	aac	tcc	gtg	cct	gtt	cgc	gtt	ggc	aat	gga	gcc	gcc					1171									
Arg	Gly	Tyr	Glu	Asn	Ser	Val	Pro	Val	Arg	Val	Gly	Asn	Gly	Ala	Ala														
			345				350					355																	
gaa	caa	tac	caa	gca	gat	gtc	gtc	ggc	gaa	gta	atg	gtc	gcg	ctt	gaa					1219									
Glu	Gln	Tyr	Gln	Ala	Asp	Val	Val	Gly	Glu	Val	Met	Val	Ala	Leu	Glu														
		360					365					370																	
acc	atc	cgc	cgc	gcc	ggg	tgc	ctc	gag	gac	gaa	ttc	tcc	tgg	ggc	atg					1267									
Thr	Ile	Arg	Arg	Ala	Gly	Cys	Leu	Glu	Asp	Glu	Phe	Ser	Trp	Gly	Met														
		375				380					385																		
caa	aaa	gcc	atc	ctc	gat	ttc	caa	gaa	gcc	aac	ttc	gac	cgc	aag	gat					1315									
Gln	Lys	Ala	Ile	Leu	Asp	Phe	Gln	Glu	Ala	Asn	Phe	Asp	Arg	Lys	Asp														
390					395					400				405															
caa	ggc	atc	tgg	gaa	atg	cgc	tcc	gaa	ccg	caa	tat	ttc	acc	cac	ggc					1363									
Gln	Gly	Ile	Trp	Glu	Met	Arg	Ser	Glu	Pro	Gln	Tyr	Phe	Thr	His	Gly														
				410				415				420																	
cgc	gcc	atg	atg	tgg	gcc	ggc	ttc	gac	cgc	ggc	atc	aaa	gcc	atc	gaa					1411									
Arg	Ala	Met	Met	Trp	Ala	Gly	Phe	Asp	Arg	Gly	Ile	Lys	Ala	Ile	Glu														
			425				430					435																	
gaa	ttc	aac	ctc	gac	ggc	ccc	atc	gag	cgc	tgg	cgt	gaa	ctc	cgc	gcc					1459									
Glu	Phe	Asn	Leu	Asp	Gly	Pro	Ile	Glu	Arg	Trp	Arg	Glu	Leu	Arg	Ala														
		440				445						450																	
aaa	ctc	cgc	gaa	gaa	atc	atg	acc	aac	ggc	ttc	aac	gaa	gag	atc	caa					1507									
Lys	Leu	Arg	Glu	Glu	Ile	Met	Thr	Asn	Gly	Phe	Asn	Glu	Glu	Ile	Gln														
		455				460					465																		
tcc	ttc	acc	cag	tgc	tac	gac	aac	acc	caa	gtc	gac	gcc	tcg	ctg	ctt					1555									
Ser	Phe	Thr	Gln	Cys	Tyr	Asp	Asn	Thr	Gln	Val	Asp	Ala	Ser	Leu	Leu														
470					475					480				485															
cag	ctc	gcc	caa	ata	ggc	ttc	atc	ggc	ttc	gac	gat	cca	aaa	atg	ctc					1603									
Gln	Leu	Ala	Gln	Ile	Gly	Phe	Ile	Gly	Phe	Asp	Asp	Pro	Lys	Met	Leu														
				490				495						500															

agc acc gta gcg cgc att gag caa gag ctt ctc gac gcc cac ggc ttt 1651
 Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe
 505 510 515

ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa 1699
 Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu
 520 525 530

tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc 1747
 Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser
 535 540 545

tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc 1795
 Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala
 550 555 560 565

gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat 1843
 Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His
 570 575 580

ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg 1891
 Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu
 585 590 595

atc agc gct gcc cgt gcc ata aat ttc gaa gaa gcg cga aac agg 1936
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<210> 382

<211> 612

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

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Leu Ser Asn Met Gly Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp
 35 40 45

Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His
 50 55 60

Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu
 65 70 75 80

Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr
 85 90 95

Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp
 100 105 110

Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp
 115 120 125

Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro
 130 135 140
 Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val
 145 150 155 160
 Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg
 165 170 175
 Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu
 180 185 190
 Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro
 195 200 205
 Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp
 210 215 220
 Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu
 225 230 235 240
 Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr
 245 250 255
 Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly
 260 265 270
 Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala
 275 280 285
 Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu
 290 295 300
 Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn
 305 310 315 320
 Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg
 325 330 335
 Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val
 340 345 350
 Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val
 355 360 365
 Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu
 370 375 380
 Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn
 385 390 395 400
 Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln
 405 410 415
 Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly
 420 425 430
 Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp
 435 440 445

Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe
 450 455 460
 Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val
 465 470 475 480
 Asp Ala Ser Leu Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp
 485 490 495
 Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu
 500 505 510
 Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly
 515 520 525
 Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val
 530 535 540
 Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met
 545 550 555 560
 Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu
 565 570 575
 Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe
 580 585 590
 Ser His Ile Gly Leu Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu
 595 600 605
 Ala Arg Asn Arg
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 <213> Corynebacterium glutamicum

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 <222> (101)..(658)
 <223> RXA01888

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 Met Ala Asp Val Ala
 1 5
 aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163
 Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp
 10 15 20
 gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc 211
 Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala
 25 30 35
 gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa 259
 Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln

40	45	50	
aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc			307
Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe			
55	60	65	
cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc			355
His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly			
70	75	80	85
ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat			403
Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp			
	90	95	100
gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta			451
Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu			
	105	110	115
gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt			499
Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu			
	120	125	130
ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc			547
Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser			
	135	140	145
gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc			595
Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu			
	150	155	160
atc gaa tta ggc cac gaa cac atc atc tac atc gat ggt ggc gac gcc			643
Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile Asp Gly Gly Asp Ala			
	170	175	180
cct ggc acc cag gaa			658
Pro Gly Thr Gln Glu			
	185		

<210> 384

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

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Ile	Val	Phe	Arg	Asp	Ala	Pro	Gly	Ala	Ser	Glu	Ser	Thr	Arg	Asn	His
		20					25						30		

Val	Lys	Glu	Lys	Ala	Ala	Glu	Leu	Gly	Tyr	Ile	Pro	Asp	Arg	Arg	Ala
	35					40						45			

Gln	Lys	Leu	Arg	Gln	Asn	Arg	Ser	Gly	Leu	Ile	Gly	Val	Ala	Phe	Glu
	50				55						60				

Met	His	Gln	Ala	Phe	His	Gly	Asp	Ile	Val	Glu	His	Leu	Tyr	Pro	Thr
65					70					75				80	

Ala	Arg	Lys	His	Gly	Phe	Asp	Leu	Tyr	Leu	Ser	Ala	Ile	Thr	Pro	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85										90					95						
Arg	Thr	Glu	Lys	Asp	Ala	Val	Asn	Ala	Leu	Ile	Arg	Glu	Arg	Cys	Glu						
			100					105					110								
Ala	Val	Ile	Leu	Leu	Gly	Ser	Arg	Met	Ser	Pro	Ser	Asp	Leu	Glu	Thr						
		115					120					125									
Ile	Ala	Gln	Gln	Leu	Pro	Val	Gln	Val	Ile	Ala	Arg	Gly	Ser	Gly	Thr						
	130					135					140										
Pro	Lys	Val	Ser	Ser	Val	His	Val	Asp	Asp	Ala	Val	Gly	Ala	Gln	Leu						
145					150					155					160						
Ala	Leu	Asn	His	Leu	Ile	Glu	Leu	Gly	His	Glu	His	Ile	Ile	Tyr	Ile						
			165					170						175							
Asp	Gly	Gly	Asp	Ala	Pro	Gly	Thr	Gln	Glu												
			180					185													

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<211> 1503

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1480)

<223> RXN01927

<400> 385

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gatgaaattt	tggatacccc	aacggaagag	gatttttaag	atg	gct	ttg	gtt	ctt		115
				Met	Ala	Leu	Val	Leu		
				1				5		

gga	atc	gat	agt	tcc	acc	caa	tcc	tgc	aag	gct	ttg	ctt	gtc	gac	gcc	163
Gly	Ile	Asp	Ser	Ser	Thr	Gln	Ser	Cys	Lys	Ala	Leu	Leu	Val	Asp	Ala	
			10					15					20			

gcc	acc	ggc	cag	gtt	atc	gac	gaa	ggc	cgc	gcg	agt	cac	ccg	agc	ggg	211
Ala	Thr	Gly	Gln	Val	Ile	Asp	Glu	Gly	Arg	Ala	Ser	His	Pro	Ser	Gly	
		25					30					35				

tcg	gag	gta	gat	cca	cgt	gcg	tgg	atc	gct	gcg	ctg	gat	caa	gct	acc	259
Ser	Glu	Val	Asp	Pro	Arg	Ala	Trp	Ile	Ala	Ala	Leu	Asp	Gln	Ala	Thr	
	40					45					50					

gag	ggg	ttg	tta	gaa	cgc	gcg	gac	gct	gta	tct	att	gca	ggc	cag	cag	307
Glu	Gly	Leu	Leu	Glu	Arg	Ala	Asp	Ala	Val	Ser	Ile	Ala	Gly	Gln	Gln	
	55					60				65						

cac	ggc	atg	gtg	gcg	ttg	gat	gaa	aac	gat	gaa	atc	gtt	cgc	ccg	gcg	355
His	Gly	Met	Val	Ala	Leu	Asp	Glu	Asn	Asp	Glu	Ile	Val	Arg	Pro	Ala	
70				75			80							85		

ttg	tta	tgg	aat	gac	act	cgt	tct	gcc	cag	gct	gcg	ttg	gat	ctc	aat	403
Leu	Leu	Trp	Asn	Asp	Thr	Arg	Ser	Ala	Gln	Ala	Ala	Leu	Asp	Leu	Asn	
			90					95						100		

gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg	451
Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val	
105 110 115	
tat gtt gct tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat	499
Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His	
120 125 130	
gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat	547
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp	
135 140 145	
ttc ctc acc tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat	595
Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His	
150 155 160 165	
ggg gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg	643
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp	
170 175 180	
cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct	691
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro	
185 190 195	
gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg	739
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val	
200 205 210	
aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt	787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu	
215 220 225	
gat ttg cag cct ggt gat gtc agc gtg tcg atc gcc acc tct ggc gtt	835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val	
230 235 240 245	
gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc	883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val	
250 255 260	
act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg	931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr	
265 270 275	
ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg	979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val	
280 285 290	
gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca	1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser	
295 300 305	
ggg ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat	1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn	
310 315 320 325	
cgt ccc gca gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc	1123
Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr	
330 335 340	

cgc gag gac ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg 1171
 Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu
 345 350 355

gat gat gct gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag 1219
 Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln
 360 365 370

cgc atc cag ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag 1267
 Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu
 375 380 385

att gcc cct gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct 1315
 Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala
 390 395 400 405

gaa tat gtg gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg 1363
 Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser
 410 415 420

ggt gag gcc acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac 1411
 Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His
 425 430 435

cgc gca cct aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt 1459
 Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg
 440 445 450

gct gca acg cag ggt tgg tac tagagctcga tattgtcgat caa 1503
 Ala Ala Thr Gln Gly Trp Tyr
 455 460

<210> 386

<211> 460

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 386

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20 25 30

Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala
35 40 45

Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser
50 55 60

Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu
65 70 75 80

Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala
85 90 95

Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp
100 105 110

Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg

115					120					125						
Trp	Met	Arg	Asp	His	Glu	Pro	Glu	Asn	Ala	Ala	Arg	Thr	Ala	Ser	Val	
130					135					140						
Met	Leu	Pro	His	Asp	Phe	Leu	Thr	Trp	His	Leu	Met	Gly	Arg	Gly	Arg	
145					150					155					160	
Lys	Val	Thr	Asp	His	Gly	Asp	Ala	Ser	Gly	Thr	Gly	Tyr	Tyr	Ser	Thr	
165					170					175						
Arg	Asp	Arg	Ala	Trp	Arg	Thr	Asp	Leu	Ala	Ala	Leu	Ala	Leu	Gly	His	
180					185					190						
Glu	Val	Glu	Leu	Pro	Glu	Leu	Leu	Ala	Pro	Asn	Ala	Ile	Ala	Gly	Thr	
195					200					205						
Thr	Pro	Gly	Gly	Val	Lys	Val	Ala	Ala	Gly	Thr	Gly	Asp	Asn	Ala	Ala	
210					215					220						
Ala	Ala	Leu	Gly	Leu	Asp	Leu	Gln	Pro	Gly	Asp	Val	Ser	Val	Ser	Ile	
225					230					235					240	
Gly	Thr	Ser	Gly	Val	Ala	Gly	Met	Thr	Val	Gln	His	Ser	Val	His	Asp	
245					250					255						
Pro	Ser	Gly	Leu	Val	Thr	Gly	Phe	Ala	Asp	Ala	Thr	Gly	Ala	Tyr	Phe	
260					265					270						
Pro	Leu	Ala	Cys	Thr	Leu	Asn	Gly	Ala	Pro	Val	Leu	Glu	Phe	Gly	Arg	
275					280					285						
Arg	Ile	Leu	Gly	Val	Glu	Trp	Glu	Glu	Phe	Asp	Ala	Leu	Ala	Leu	Ala	
290					295					300						
Ala	Gln	Pro	Gly	Ser	Gly	Gly	Val	Thr	Leu	Gln	Pro	Tyr	Leu	Glu	Gly	
305					310					315					320	
Glu	Arg	Thr	Pro	Asn	Arg	Pro	Ala	Ala	Arg	Gly	Val	Leu	Ala	Gly	Leu	
325					330					335						
Asn	Cys	Ala	Thr	Thr	Arg	Glu	Asp	Phe	Ala	Arg	Ala	Thr	Val	Glu	Gly	
340					345					350						
Leu	Leu	Leu	Ala	Leu	Asp	Asp	Ala	Val	Thr	Ala	Leu	Val	Glu	Ala	Thr	
355					360					365						
Gly	Val	Pro	Val	Gln	Arg	Ile	Gln	Leu	Ile	Gly	Gly	Gly	Ala	Arg	Ser	
370					375					380						
Gln	Ala	Val	Arg	Glu	Ile	Ala	Pro	Glu	Ile	Phe	Gly	His	Glu	Ile	Val	
385					390					395					400	
Val	Pro	Glu	Pro	Ala	Glu	Tyr	Val	Ala	Leu	Gly	Ala	Ala	Arg	Gln	Ala	
405					410					415						
Ala	Trp	Ala	Leu	Ser	Gly	Glu	Ala	Thr	Pro	Pro	Gln	Trp	Pro	Thr	Pro	
420					425					430						
Gly	Ser	Asp	Pro	His	Arg	Ala	Pro	Lys	Asn	Thr	Glu	Leu	Ser	Thr	Arg	
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Tyr Ala Lys Leu Arg Ala Ala Thr Gln Gly Trp Tyr
 450 455 460

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 <212> DNA
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<220>
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 <222> (1)..(1116)
 <223> FRXA01927

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 ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg tat gtt gct 96
 Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
 20 25 30
 tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa 144
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
 35 40 45
 aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc 192
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
 50 55 60
 tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct 240
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65 70 75 80
 tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat 288
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
 85 90 95
 cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg 336
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
 100 105 110
 gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct 384
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
 115 120 125
 gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag 432
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu Asp Leu Gln
 130 135 140
 cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg 480
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
 145 150 155 160
 acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc act ggt ttc 528
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
 165 170 175
 gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc 576

Ala	Asp	Ala	Thr	Gly	Ala	Tyr	Phe	Pro	Leu	Ala	Cys	Thr	Leu	Asn	Gly		
			180					185					190				
gca	ccg	gtg	ttg	gaa	ttc	ggc	cgc	cgc	att	ctg	ggc	gtg	gaa	tgg	gaa	624	
Ala	Pro	Val	Leu	Glu	Phe	Gly	Arg	Arg	Ile	Leu	Gly	Val	Glu	Trp	Glu		
		195					200					205					
gag	ttc	gat	gcg	ctt	gca	ctg	gct	gct	caa	ccc	ggc	tca	ggc	ggc	gtg	672	
Glu	Phe	Asp	Ala	Leu	Ala	Leu	Ala	Ala	Gln	Pro	Gly	Ser	Gly	Gly	Val		
		210				215					220						
acg	ctc	cag	cct	tat	ttg	gag	ggc	gag	cgt	acg	ccg	aat	cgt	ccc	gca	720	
Thr	Leu	Gln	Pro	Tyr	Leu	Glu	Gly	Glu	Arg	Thr	Pro	Asn	Arg	Pro	Ala		
225					230					235					240		
gca	cgt	ggc	gtt	ttg	gct	gga	cta	aac	tgt	gca	acg	acc	cgc	gag	gac	768	
Ala	Arg	Gly	Val	Leu	Ala	Gly	Leu	Asn	Cys	Ala	Thr	Thr	Arg	Glu	Asp		
			245					250						255			
ttt	gcc	cga	gca	act	gtt	gaa	ggc	ttg	ttg	ttg	gca	ttg	gat	gat	gct	816	
Phe	Ala	Arg	Ala	Thr	Val	Glu	Gly	Leu	Leu	Leu	Ala	Leu	Asp	Asp	Ala		
			260					265						270			
gta	acg	gcg	ctg	gtt	gag	gcc	acg	gga	gtg	ccc	gtt	cag	cgc	atc	cag	864	
Val	Thr	Ala	Leu	Val	Glu	Ala	Thr	Gly	Val	Pro	Val	Gln	Arg	Ile	Gln		
		275					280					285					
ctc	atc	ggc	ggc	ggc	gcg	cgt	tca	cag	gcg	gtt	cgt	gag	att	gcc	cct	912	
Leu	Ile	Gly	Gly	Gly	Ala	Arg	Ser	Gln	Ala	Val	Arg	Glu	Ile	Ala	Pro		
		290				295					300						
gag	att	ttc	ggc	cat	gag	att	gtg	gtt	cca	gaa	ccc	gct	gaa	tat	gtg	960	
Glu	Ile	Phe	Gly	His	Glu	Ile	Val	Val	Pro	Glu	Pro	Ala	Glu	Tyr	Val		
305					310					315					320		
gcg	ttg	ggc	gca	gct	cgt	cag	gcg	gca	tgg	gcg	ctg	tcg	ggc	gag	gcc	1008	
Ala	Leu	Gly	Ala	Ala	Arg	Gln	Ala	Ala	Trp	Ala	Leu	Ser	Gly	Glu	Ala		
			325						330					335			
acg	cca	ccg	cag	tgg	cca	act	ccc	ggc	tcc	gat	ccg	cac	cgc	gca	cct	1056	
Thr	Pro	Pro	Gln	Trp	Pro	Thr	Pro	Gly	Ser	Asp	Pro	His	Arg	Ala	Pro		
			340					345					350				
aaa	aac	act	gag	ctg	agc	acg	cgt	tat	gcg	aag	ctg	cgt	gct	gca	acg	1104	
Lys	Asn	Thr	Glu	Leu	Ser	Thr	Arg	Tyr	Ala	Lys	Leu	Arg	Ala	Ala	Thr		
		355					360					365					
cag	ggc	tgg	tac	tagagctcga	tattgtcgat	caa										1139	
Gln	Gly	Trp	Tyr														
		370															

<210> 388

<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

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 20 25 30
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
 35 40 45
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
 50 55 60
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65 70 75 80
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
 85 90 95
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
 100 105 110
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
 115 120 125
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln
 130 135 140
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
 145 150 155 160
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
 165 170 175
 Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly
 180 185 190
 Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu
 195 200 205
 Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val
 210 215 220
 Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala
 225 230 235 240
 Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp
 245 250 255
 Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala
 260 265 270
 Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln
 275 280 285
 Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro
 290 295 300
 Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val
 305 310 315 320
 Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala
 325 330 335
 Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro

340 345 350
 Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr
 355 360 365
 Gln Gly Trp Tyr
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 <213> Corynebacterium glutamicum
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 Met Asp Ser Pro Met
 1 5
 agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc 163
 Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala
 10 15 20
 gat ctc acc gca aaa gtt caa cgc cac cct gaa cct gga gaa acc ctc 211
 Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu Pro Gly Glu Thr Leu
 25 30 35
 ctg ggt agc ggc ggc aca gtg agt gct ggt ggc aaa ggc gcc aac caa 259
 Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly Lys Gly Ala Asn Gln
 40 45 50
 gct gtg gcg gca gcg caa tta ggt gcc aaa gtc acc atg atc ggt gcg 307
 Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val Thr Met Ile Gly Ala
 55 60 65
 gtc gga acc gat caa atg gct ggc gag gcg ctg aca cat ttg cgt caa 355
 Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu Thr His Leu Arg Gln
 70 75 80 85
 tca gga gca gat atg tcc gcg att gcc act gtg gac ggt ccc act ggt 403
 Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val Asp Gly Pro Thr Gly
 90 95 100
 ctt gcc atc atc act gtg tct gac gat ggg gaa aac acc atc atc gtt 451
 Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu Asn Thr Ile Ile Val
 105 110 115
 atc cct ggc gct aac gct tct gtc acc gcg gaa ttt gtt gat aaa cac 499
 Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu Phe Val Asp Lys His
 120 125 130
 tcc caa ctc att gag aac gcc ggc att gtg ttg ctt cag ggt gag atc 547
 Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu Leu Gln Gly Glu Ile
 135 140 145